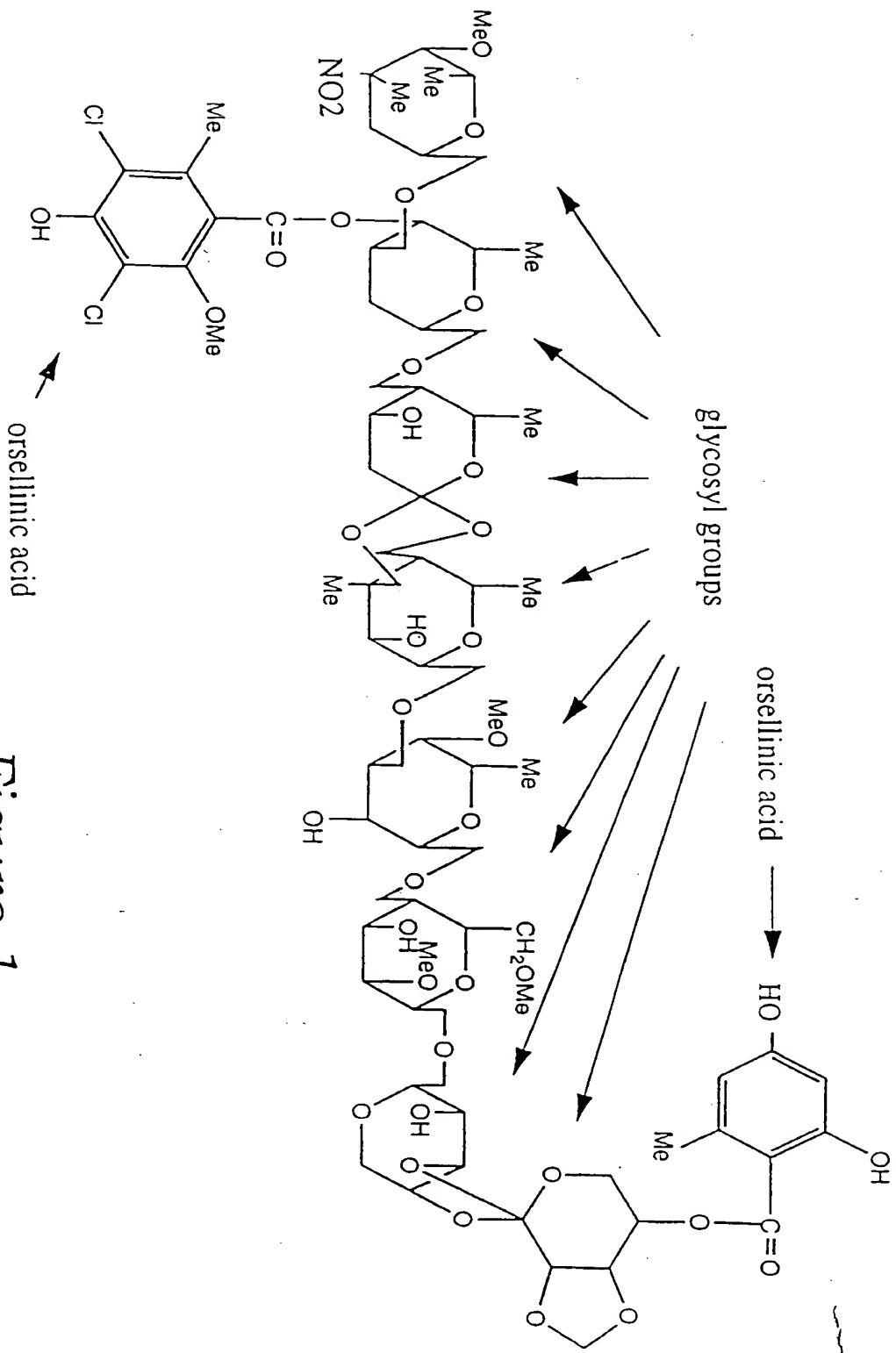Structure of everninomicin (Ziracin)

Figure 1

Overlapping cosmids and clones spanning 185 kb of chromosomal DNA containing the Everninomicin Pathway region.
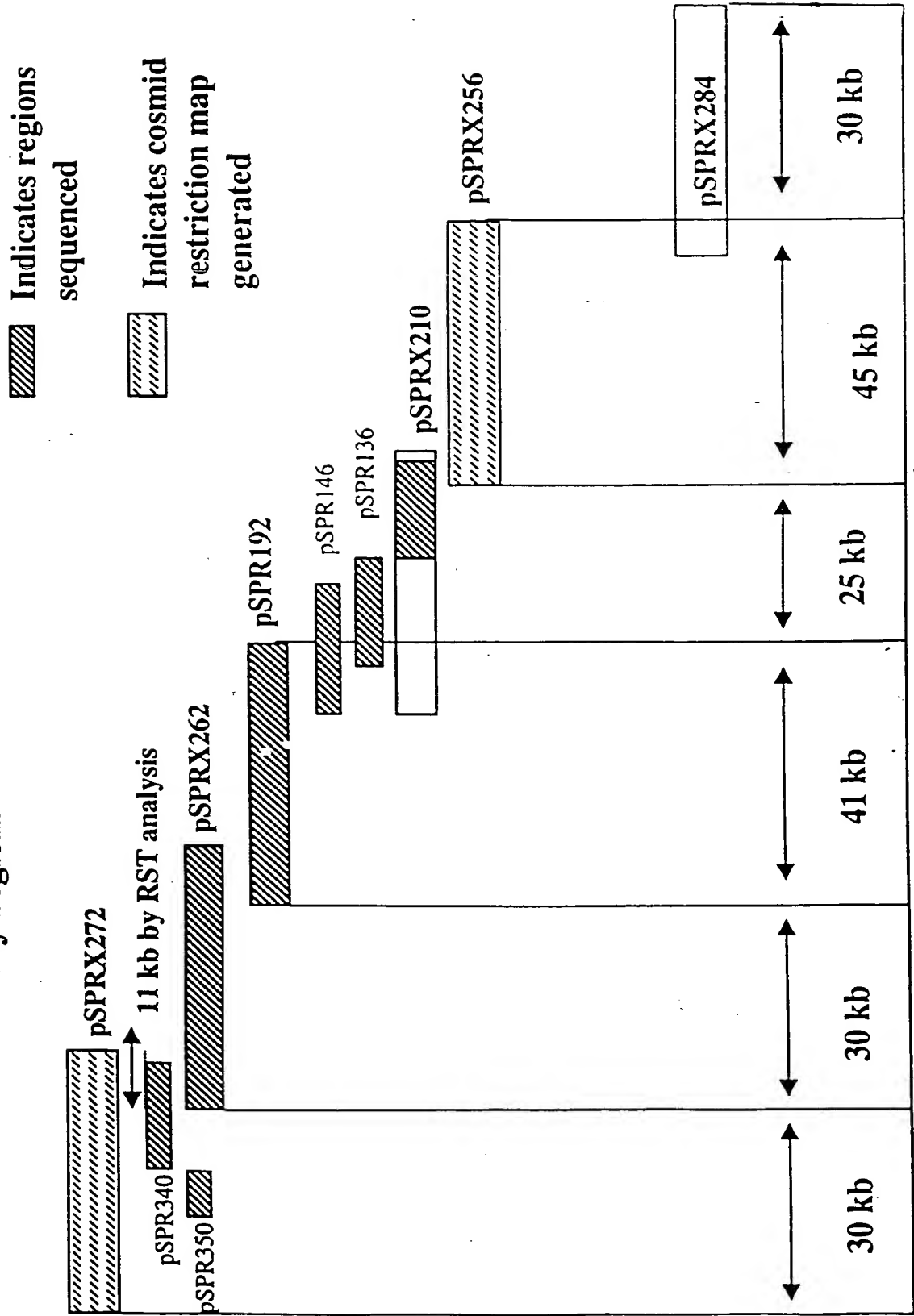
Figure 2A

pSPRX272
37.5kb

Cosmid pSPRX272

Regions sequenced indicated by crosshatches.

Fragments cloned indicated by clone designation benigth fragment.

pSPR272
(37500 bp)
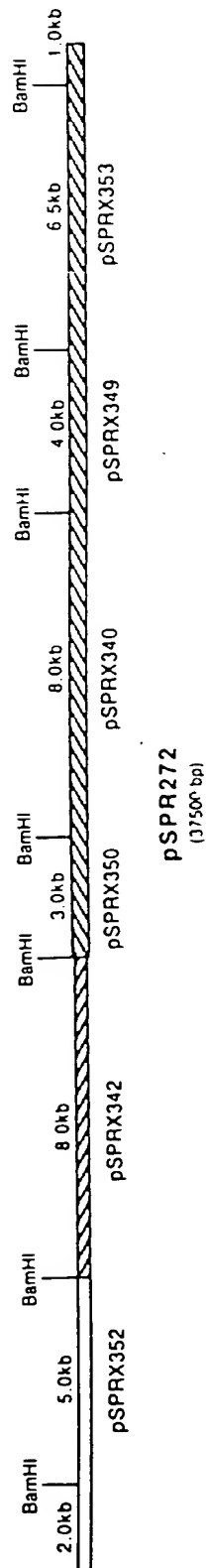
Figure 2B

Cosmid pSPRX256

Regions sequenced indicated by crosshatches.

Fragments cloned indicated by clone designation benigth fragment.

Cosmid
pSPRX256

| Kpnl | Kpnl | Kpnl | Kpnl | Kpnl | Kpnl | Kpnl | Kpnl | Kpnl |
| 2.15kb | 8.0kb | 1.6kb | 4.3kb | 5.0kb | 5.5kb | 5.0kb | 5.0kb | 4.3kb | 4.6kb |

pSPRX369
left edge   pSPRX367   pSPRX361   pSPRX365   pSPRX501   pSPRX502   pSPRX363   pSPRX369
                                                                                      right edge

pSPR256 Map.patent
(425 bp)
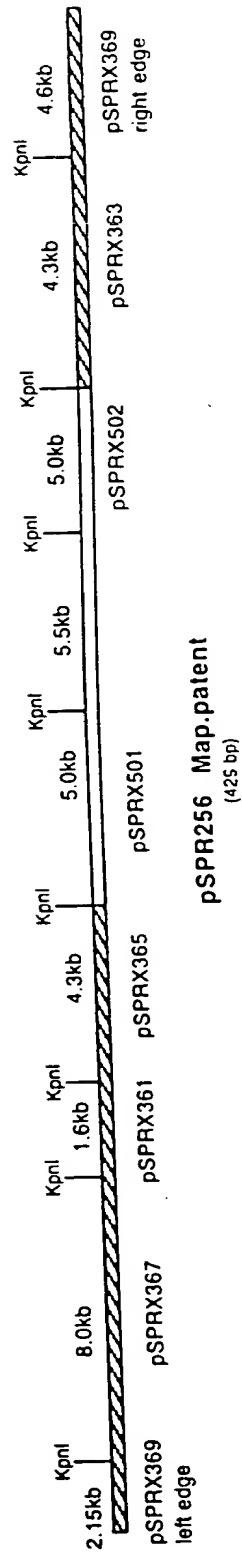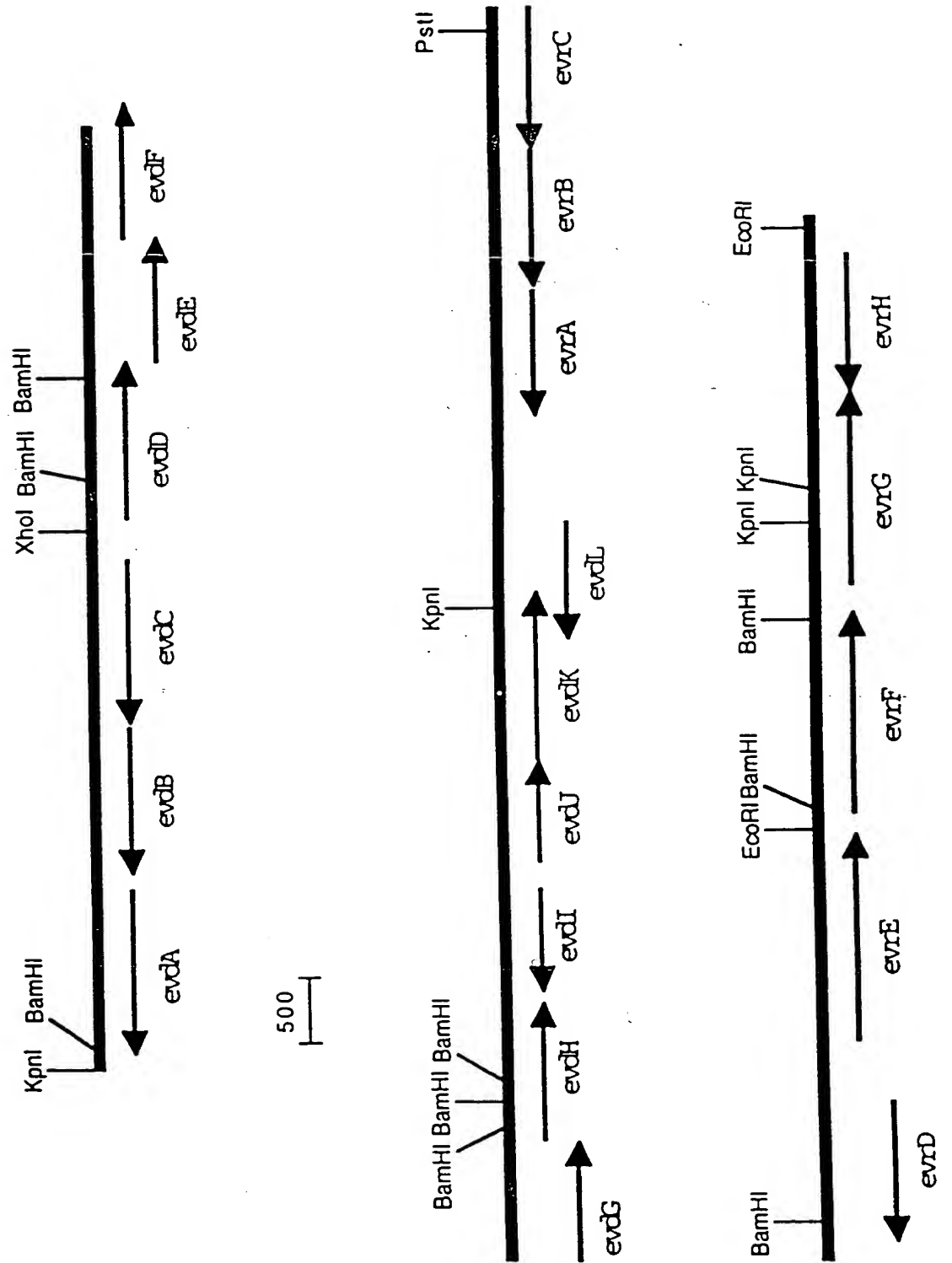
Figure 2C

Figure 3 (A)

Figure 3 (B)
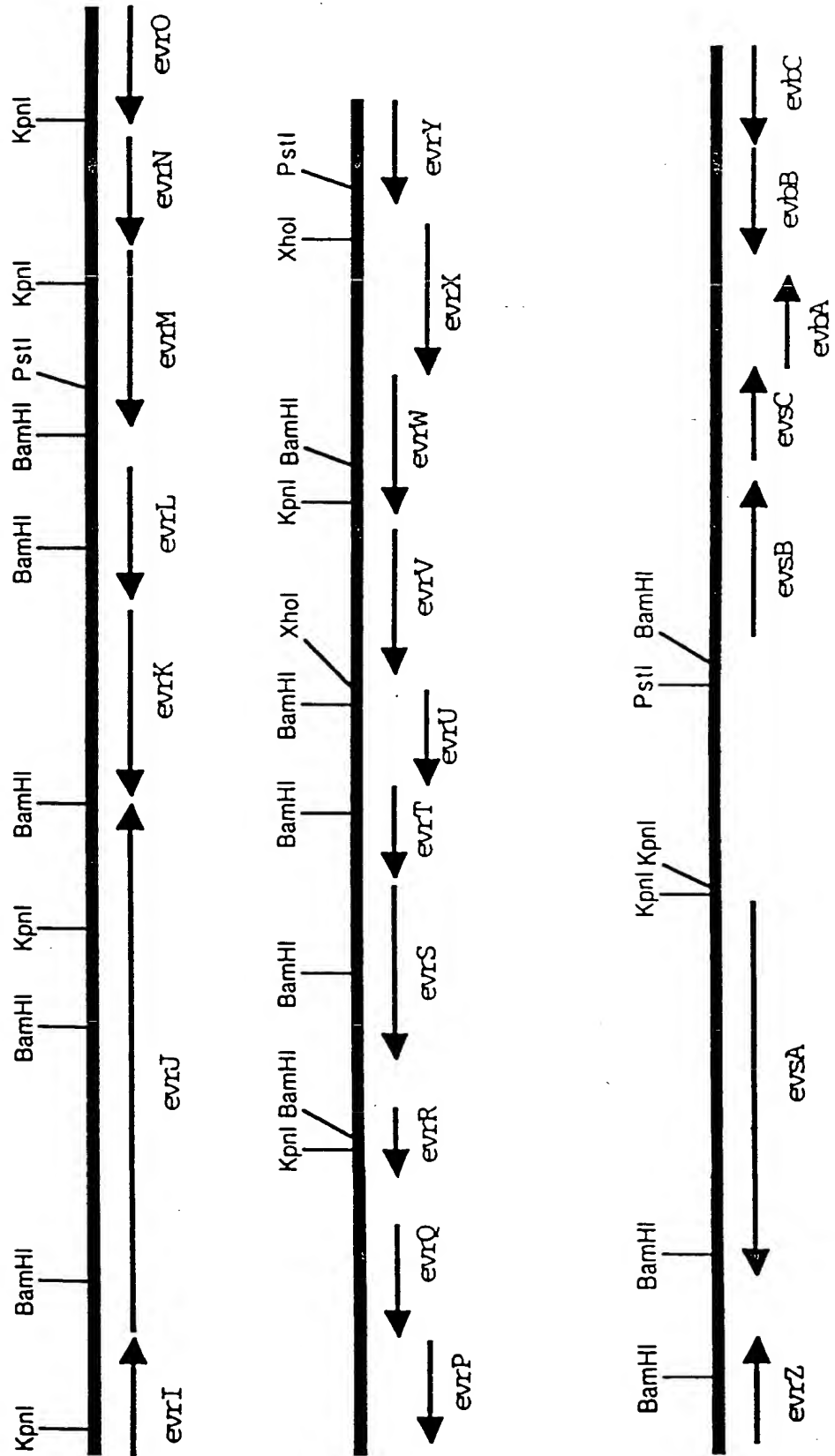
Figure 3 (C)
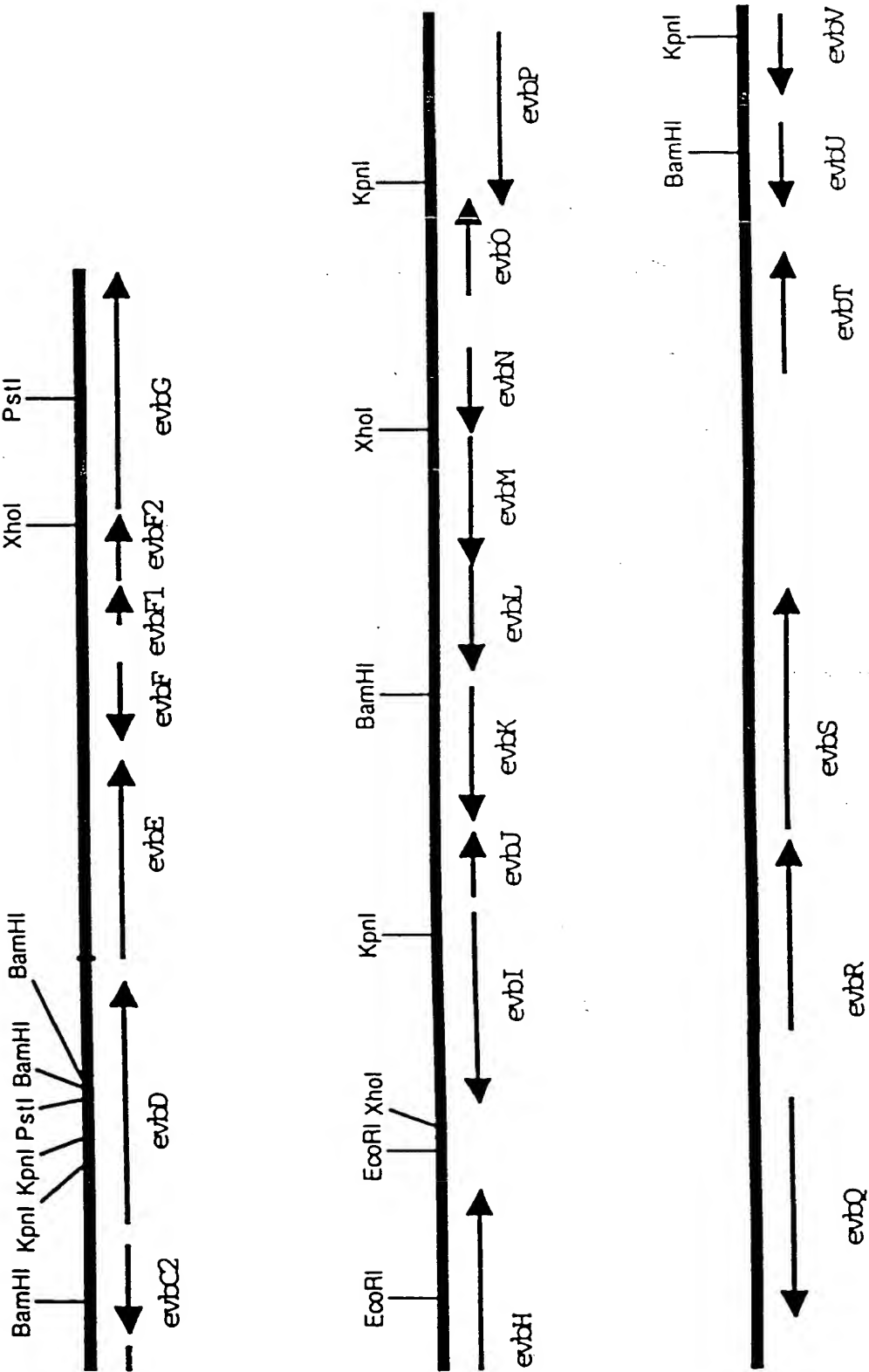
Figure 3 (D)

Figure 4(A)

Figure 4 (B)

Figure 5 (A)

D-glucose-1-phosphate

glucose-1-P-nucleotidyl-
transferase

EvrX

NDP-D-glucose
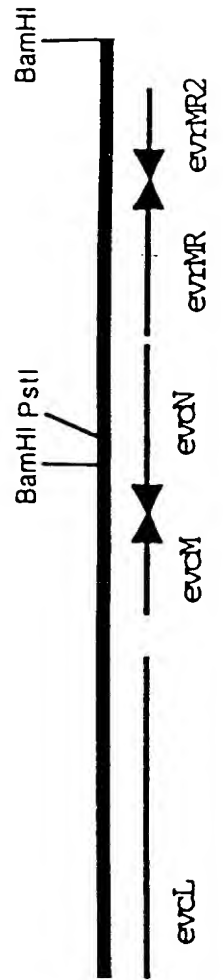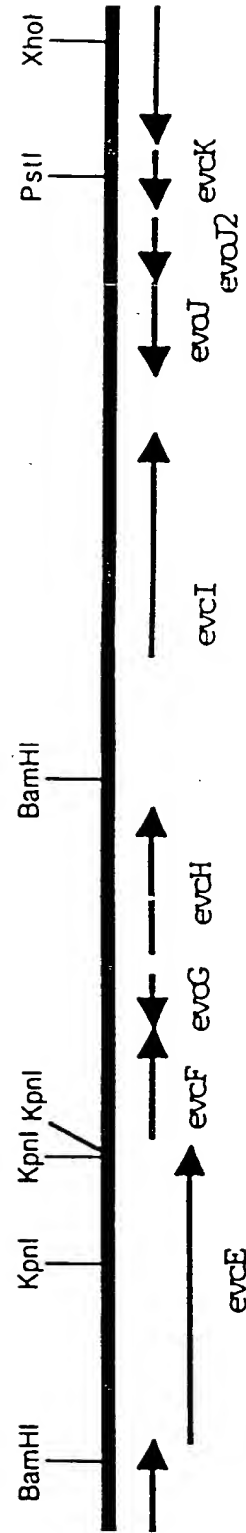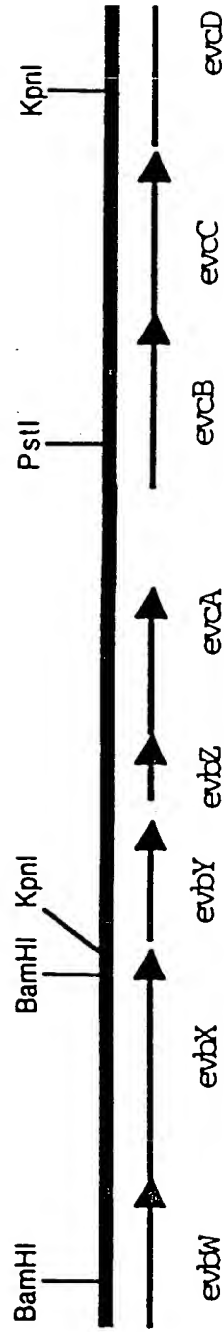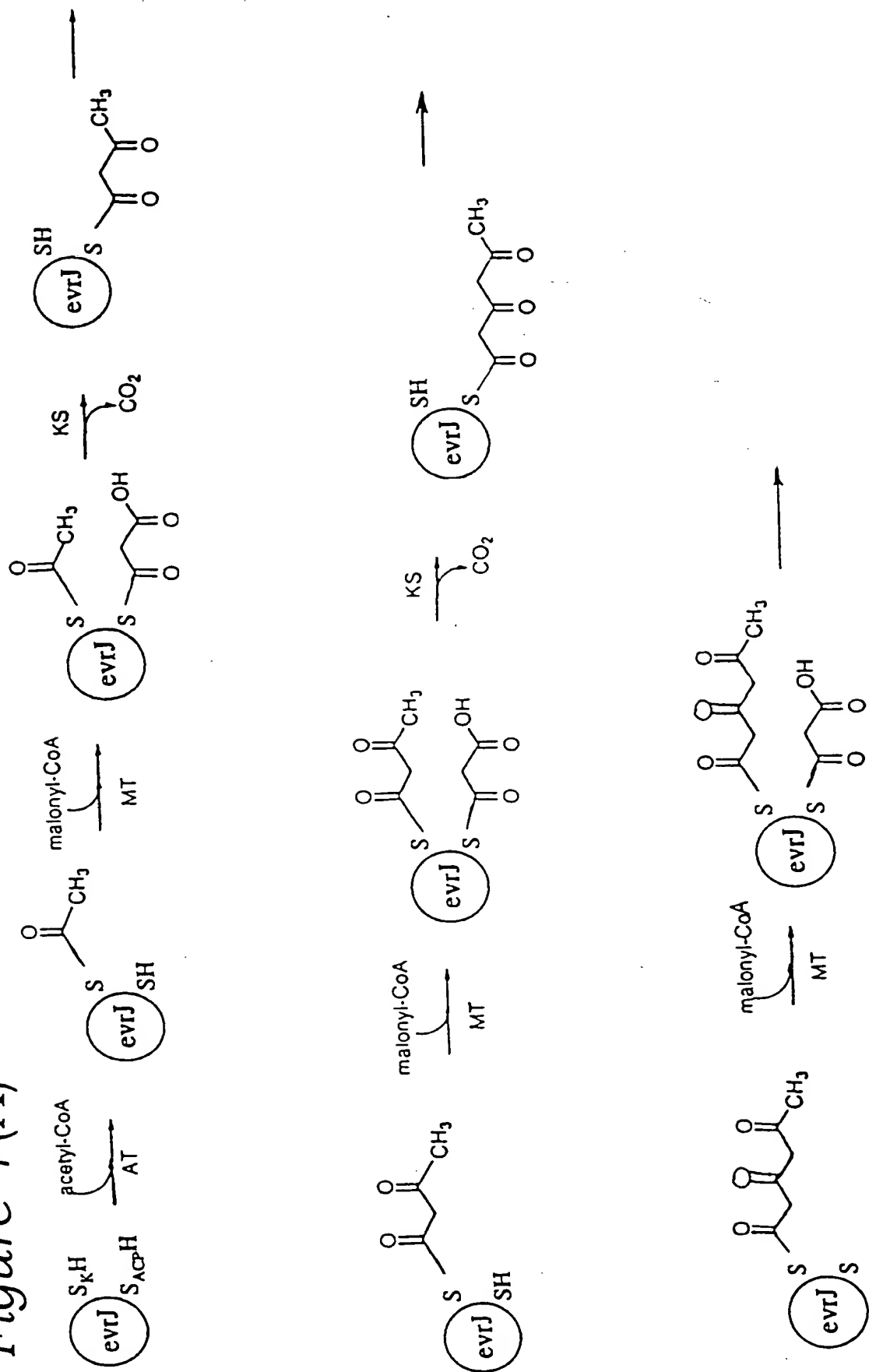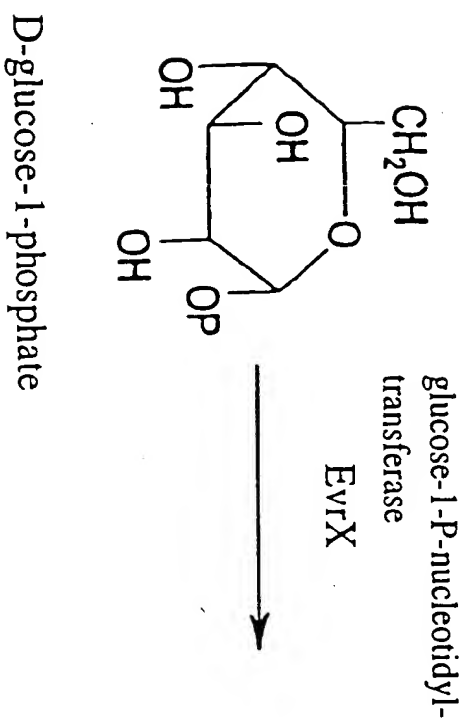
NDP-glucose-4-6-
dehydratase

EvrW

Figure 5 (B)

NDP-4-keto-6-deoxyglucos
3,5 epimerase

EvrV

NDP-4-keto-6-deoxy-
D-glucose

NDP-4-keto-rhamnose

Modifications and
Glycosyltransferase
attachment
to Everninomicin
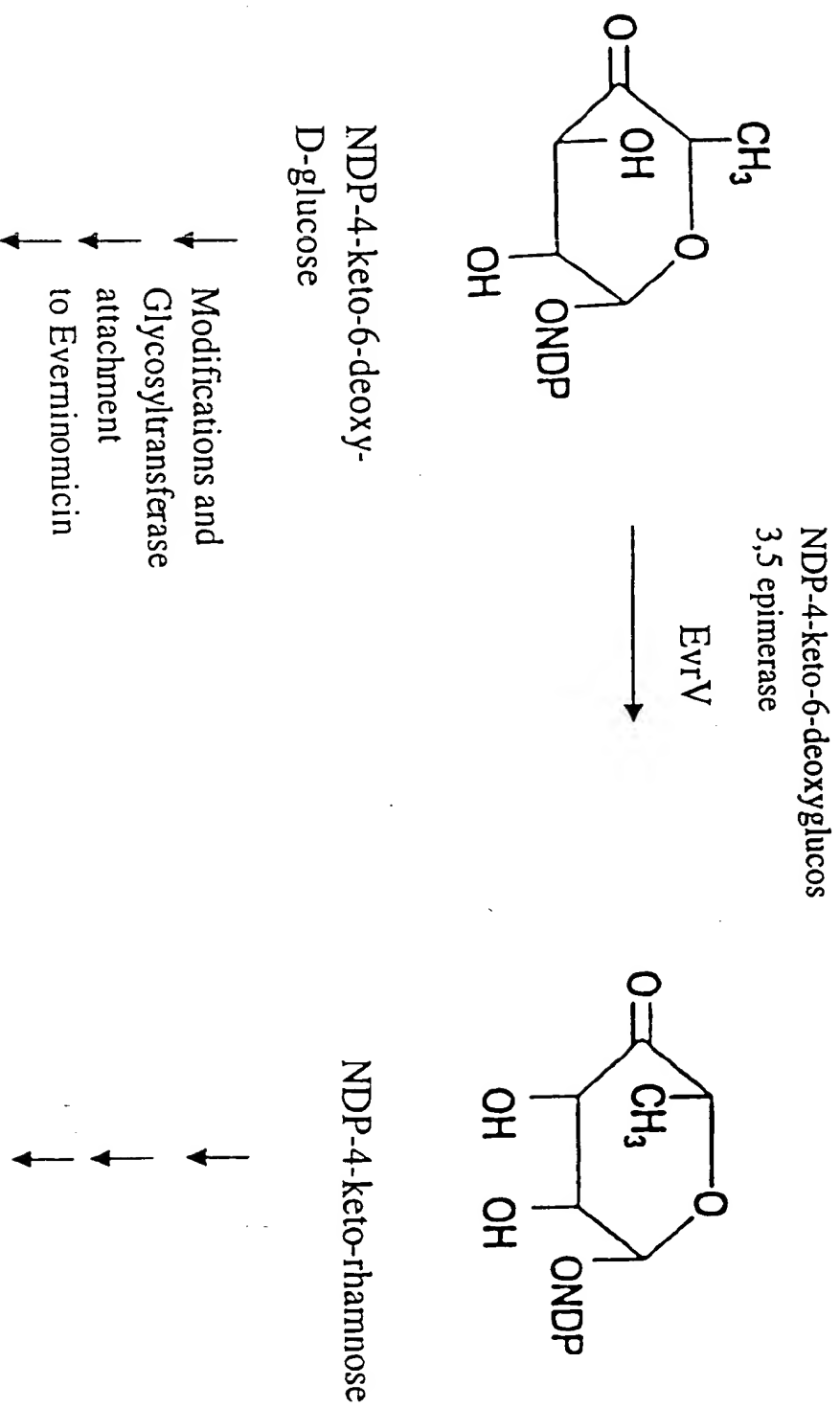
pSPRH830b *E.coli*-Micromonospora shuttle vector

Figure 6
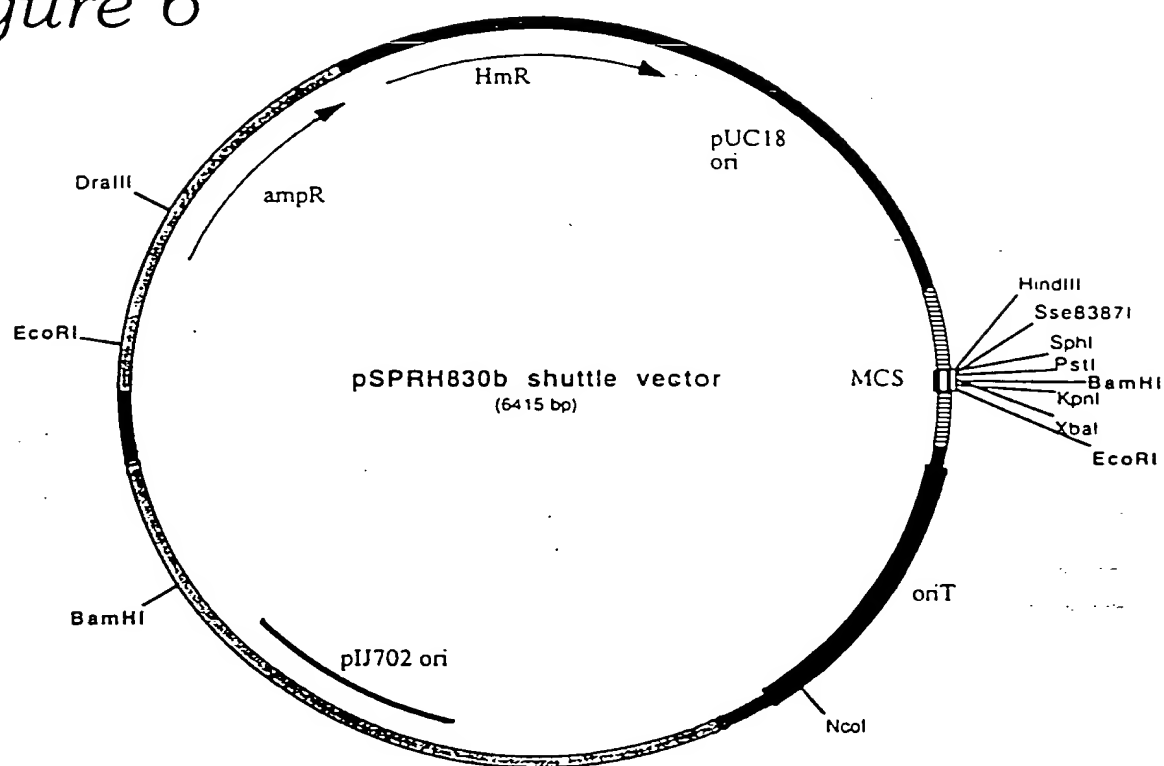
pSPRH830b - pSPRH826b backbone

Function	Source
- Ampicillin resistance	(pUC18)
- Multiple cloning site	(pUC18)
- pUC18 origin	(pUC18)
- Hygromycin resistance	(p16R1)
- oriT (origin of transfer)	(pRL1058)
- pIJ702 origin of replication	(pIJ702)

pSPRH840 integrating vector

Figure 7A

Hygromycin Resistance

pSPRH840
(7098 bp)

xis

integrase

oriT

inverted repeat

attP

pSPRH840 - pSPRH826b backbone, pMLP1 *xis, int* attP insert

pSPRH840 conjugated from *E. coli* into	HmR transformants obtained
M.carbonacea	+
M.rosaria	-
M.halophitica	+

```
   1 GTACCTCGCCTTGATCGTGCCGGGTGGCCGGCTCGGCCGGCTGG...GTCGTGTCGGGTAGGGTCTGGGACATCTGGACTCCTTGCTTGCGGTAGG.CT...CGGGTGGGAGCCCT
 117 GGCCGGTGGTGCGGCTGGGGGCTCGTCTGCGTCAGGCCGCAGCAGCCCGGCGTGGTCCGCCGGCGGC.TGGGC.TTGATCGGTCCGGCCGGGGGCT.CGCCGCCCTCGGCGGGT.TG
 233 GTGGGGCGCGGAGGGGGAGAGCTCGGCTTTTTCGGCCCGAAGATGCCCAGCACGGGGGCCGCGTCGGGTCGCTCCTTCTTGCTCTCAAGCCACGCAGCGATGTCGTCCTCGTCGAA
 349 GCCGGGCGCGCCGGCCGACCTCAGGTGATCGGCAGGGTCCGGGCGGGTGATGGCGTCGCGAACTCAGGTCACCTCGACGCCGAGCGCGGCGGCGAGCTGCTCCTTGTTCATCAGCGGCT
 465 TCATGCGGCGGCCTCGAACAGGTCCTCGACCTTGGTGCCGAGGCGGTCGGCCATGTGCAGGGCCAGCTCAAGGCTCGGGGTCTGCCCCTTGCGGATGCGCAGCAGATTGACCCGAT
 581 CCATGCCGCACAGTCGCGCCCGAGCGCGCGTTGGTCGTGGCGCCCACGTTCGGCGGGCGAGGCGGTCGAAGACGTCAGTGCGTAGCCGAATCCGCGATGCGCACACGTATGCCGCGGATTG
 697 ATCTCGGGAGGTGCTGCACTCATGTCGCAAGCCTAGGGTGCTGCACTCGTGTCGCACCCTCGTACTTTCGGCCCGATTCTGACCCGCCCTCCAGGACCCTACTGTTGCATCAGTGCA
 813 ACACCTATGAAGGGAAGCAAGATGCCCGGCCAGAGAGGGATGGCCGGTAGGCAAGCGACGATCAAGCATGTGGAGCGCAGTGGGTGTTGCGCAAAGGCAACGCGACAGGTCCGCAACC
 929 GGTCCGACCTGCCGGTTACGACCTACGGTGTGCAC ATG CGCAACACACCGGGGCTGGGGCGCGGCACATGGGCCGCATACGTCCTCACTGCCTCGCGAGCGCGCGCGGACTGACCAAG
      1▸ M  R  N  T  P  G  L  G  R  G  T  W  A  A  Y  V  L  T  A  R  E  R  A  G  L  T  K
1044 AGCGAGTTGGCCAGGCGCATCCAGAAGGACCGGGCCCACCGTCGGCCGGTGGGAGGACGGCAAGAACTCGGCCCTGACGACGCGGACCTCGTTGCCCGCGTCGCCCAGGTCGCTCGGCCT
  28▸ S  E  L  A  R  R  I  Q  K  D  R  A  T  V  G  R  W  E  D  G  K  N  R  P  D  D  A  D  L  V  A  R  V  A  Q  V  L  G  L
1160 CGACCTCGACGAAGCCCTCGCCGCCGCAGGTCTGCGCCCCGGCCGTCACCCCGCCAGCGACCCCAACCATGGACCTGGACGAGGAAATCGAGCTGGTCCGCACCGACCCCAAGCTGG
  66▸ D  L  D  E  A  L  A  A  A  G  L  R  P  G  V  T  P  P  A  T  P  T  M  D  L  D  E  E  I  E  L  V  R  T  D  P  K  L
1276 ACGAGGACATGAAGCGGCGCATCATCGCCCTAATCCTGGAGCGCGCCGTGAGCGCGACAAGGCGGCGGCGATCGAGGAAACCAAGCGGCTCATCGACCTGTTCCGCCGCAGC TGA CA
 105▸ D  E  D  M  K  R  R  I  I  A  L  I  L  E  R  R  E  R  D  K  A  A  A  I  E  E  T  K  R  L  I  D  L  F  R  R  S  ·
1391 ACG GTG TCGGATCGAGAAGAACGGGCCCGTCTACCGCATTCGGGACCTCGTTCGCGGTAAAAAGGTCACCATTCAGACCGGTTATCCGACGAAGACCAGCGCCAAGAATGCGATGG
   1▸ V  W  I  E  K  N  G  P  V  Y  R  I  R  D  L  V  R  G  K  K  V  T  I  Q  T  G  Y  P  T  K  T  S  A  K  N  A  M
1506 TGCAGTTCCGTGCGGAGCAGTTGCAGGGCAACGCGCTCATGCCGCGCGGCGGTCAGATTACCCTCGCCGATTTCGTGGGGGAGTGGTGGCCGAGCTACGAAAAGACGCTGAAACCG
  38▸ V  Q  F  R  A  E  Q  L  Q  G  N  A  L  M  P  R  G  G  Q  I  T  L  A  D  F  V  G  E  W  W  P  S  Y  E  K  T  L  K  P
1622 ACCGCCGTGAACTCGGAGGGCAACGGATCCGCAACCACCTCCTGCCCATACTCGGCCATCTCACCCTTGACGAGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAACGACCTGGA
  77▸ T  A  V  N  S  E  G  N  R  I  R  N  H  L  L  P  I  L  G  H  L  T  L  D  E  L  D  G  Q  V  T  Q  Q  W  V  N  D  L  E
1738 GGCCGGCGTCGGCCCGTGGCCGGAGTCCACGCGGGGTCGTCGGAAGCCGCTGGCAGCGAAGACGATCAGCAACTGCCACGGCCTGCTGCACACGATCTGCGGCGCGGCGATCGCGG
 115▸ A  G  V  G  P  W  P  E  S  T  R  G  R  R  K  P  L  A  A  K  T  I  S  N  C  H  G  L  L  H  T  I  C  G  A  A  I  A
1854 CGAAACGGATCAGGCTCAACCCGTGCTCTTCGACGATGCTGCCCCGGCGCGAGCCGAAAGAGATGAAGTTCCTGAGCGACCCGGAGATCGGTCGGCTTATCACGGCGCTTCCGCCG
 154▸ A  K  R  I  R  L  N  P  C  S  S  T  M  L  P  R  R  E  P  K  E  M  K  F  L  S  D  P  E  I  G  R  L  I  T  A  L  P  P
1970 CACTGGCGACCGGCTCGTCATGCTGCTGGTGGCGACCGGTCGTGAGGTGGGGTGAGGCGATCGGCCTGCGCGGCCGGCCGGGTCGACCTGCTCGCCGCGCGCCCCGGCTGACCGTCGT
 193▸ H  W  R  P  L  V  M  L  L  V  A  T  G  L  R  W  G  E  A  I  G  L  R  A  G  R  V  D  L  L  A  A  R  P  R  L  T  V  V
2086 CGAGCAGCTCCAGGAGCTGGCCAGCACGGGAGAGCTCGTCTTCCAGTCGCCGAAGACCGCGAAGGGCCGGCGCACGGTCAGTTTCACCACGAAAGTCGCTCTACTGCTTACGCCAC
 231▸ E  Q  L  Q  E  L  A  S  T  G  E  L  V  F  Q  S  P  K  T  A  K  G  R  R  T  V  S  F  T  T  K  V  A  L  L  L  T  P
2202 TCATCGCCGGAAAGAAAAGTGACGAGGTCGTGTTCACCGCGCCGAAAGGCGGGATGGTAAGGACGCGCAATTTCCGGCGGATCTGGGTCAAGGCGTGCGAGGAAGCCGGGCTTCCG
 270▸ L  I  A  G  K  K  S  D  E  V  V  F  T  A  P  K  G  G  M  V  R  T  R  N  F  R  R  I  W  V  K  A  C  E  E  A  G  L  P
2318 GGCTTACGCATTCACGATCTGCGGCACACTCACGCGGCGGATCCTGATTTCTGCCGGGCGTCGGCTGTCGGCGATCTCCCGCCGCCTCGGTCACTCGTCGATCGCGGTGACGGATCT
 309▸ G  L  R  I  H  D  L  R  H  T  H  A  A  I  L  I  S  A  G  R  P  L  S  A  I  S  R  R  L  G  H  S  S  I  A  V  T  D  L
2434 GCTGTACGGGCACCTGCGTGAGGAGGTCGACGAGGGGATCCTCGCGGCGATCGAGGAGGCGATGGCCGGCGTCCGGGCTGAGGACCTGCAGGCGGAACTCGACGAGGAGCTGACGG
 347▸ L  Y  G  H  L  R  E  E  V  D  E  G  I  L  A  A  I  E  E  A  M  A  G  V  R  A  E  D  L  E  A  E  L  D  E  E  L  T
2550 ACGTGTTGGCCGACGCAGCA TGA TCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCCAATCCGGAGCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGT
 386▸ D  V  L  A  D  A  A  ·
2665 TGACCCCCTGACCAGGGCCCCGGTA CGGGTTCAATTCCCATCAGTCACCCG GCAAGTCGGATCTACTCCACAGCAGATCAGGCCCCCTCCGAAGAGGGGGCCTG
2768 ATGCGTCATAGGGGACAGGTAGGGGAACTCAACCCCCGGCTCCTTGCTCGCGTCGGGTCATGCCGTCCGCGTACCCCTCCGCGTACCTGGCCCTCTCCCGTTCCTCGATCTCGGCG
2884 GCGAGCTGATCGCGCAGGTCGCGCCTCCATCGCCTGCCGGCGTTCGGCCGTCTCGCTCGAGGCCAGGACCCCGGCGCCACTCCGACCGCCCCGCCGGGCGGGCATGGCCGGATCCGCG
3000 CCAGGCGGCGAACGCCTCCGTCACGGCCTCCAGCCGCACCCGCTCCAGCTCCGTCTGGTGCCGGCGCTCGTCCGCCTCGATGTCGGCGGCCATCGACTCGATGACGTCCTGGTAGT
3116 GCTCCCGCTCGTGCTGCCACTCGTCGCGCTCGGCGCGGCGCAGCGCCTGGCACGTGCAAGCGACGGCGACGCCGACGACAGCGGCGAGGGTGCAACGATCGATCATCGTGCTCATC
3232 ATGGGTCCGTCTCCGATCAGCGACCCCGGCGGGCGGCGTCGAGCGGAGGGGTGATCGTTTCGAGATGGATGTACACCGGCGTACTCCTCACGTTGGAGACTCGCCTCGATCAGACA
3348 CCCGTTCGACTGGTGACCGAAAGCCCTGCTCGGGGACACTCCACGCACCACCGGACGACTGGTGGTGCGTGAACTTCCACGTGGTAAGGGGTTACTCAGAGTGCATGTTTCATAGGG
3464 TGGGCGCCGGTCGACAATGACGTAGAGTGGCCTTACCATGCACTTCCGTCGATATTGAGCTGTGCGTTACCGGTGCGTAACCTGGACGGCAATTCCAGATTGCGGGCGAACACGCG
3580 AAACCCGGATCAGGCGCGCGGAATGCGCACGCCTACCTCATCCGCCGGATATACATCCATCAGCCCGTCCGGATTGCGCACCACCAACACCGGCACACCCTCGGGGATGTTCATCTC
3696 CGCTCGCTCCTCCGGCGTGGGCATCGGGGCCATGACGAACTGGTCCGGCTCGCCCACCAGCTCGTCGAGTTCGACGGCCCCCGCACCCGCGTGCCTCGCCCCGGAGGCGGCGTCGA
3812 CGAGTCCCTCAGCCGCGCAGCTCGGCGACCGCCCGTCGCACGGTGCCCCTGCCCACCCCGTACTCCTGGCTCAGCCGCAGTCTCGCTGGGCAGCAGCCGCCCGCAGCGTACGTGCCG
3928 TCCTGGATGCCGGGCGCGCAGCAGCGCGGCTCAGCTGGAGGGCGGCGGGCACACTGGAGTGCGGGCTGATCACAGGCCGGACGGTAGGGATGCCGGGGGCGGACGTTCGCCCGGCGCAA
4044 CGTTCGAACGTTCGGTGCGCTCTATGCCTCGGCCACGTATACCCCTGCTCCGGCGCGGCCCACGGTAAGCCCGCCGGTCCCGGGTGAGCTCCAGGGCGCGCTGGATGTCGACACGC
4160 TGACCGAGTACAGATCGGCCAGCTCTCGCAGCGACGGGAGCTTCGACCCGGGCCGGGTACTCGCTGCTGCGGATCGGGCCGGTCAGGTCGTCGGCGATCTGGCGCGACGACATGGGG
4276 ATGGGCATGGCCGGATCTCCCTGGTTGGCCCGGCCGATGACGATCACGCCCGCCACGCTGCCTCAAGCAGTGATTGACCAGTAGTCACACAGTGACCTAGGTTGGCCGATGGGTAC
```

Figure 7B

Figure 8

pSPRH826b final construct
(4559 bp)

AmpR

MCS

HindIII (1035)
SphI (1041)
Sse8387I (104€
PstI (1047)
XbaI (1059)
BamHI (1065)
KpnI (1074)

HmR
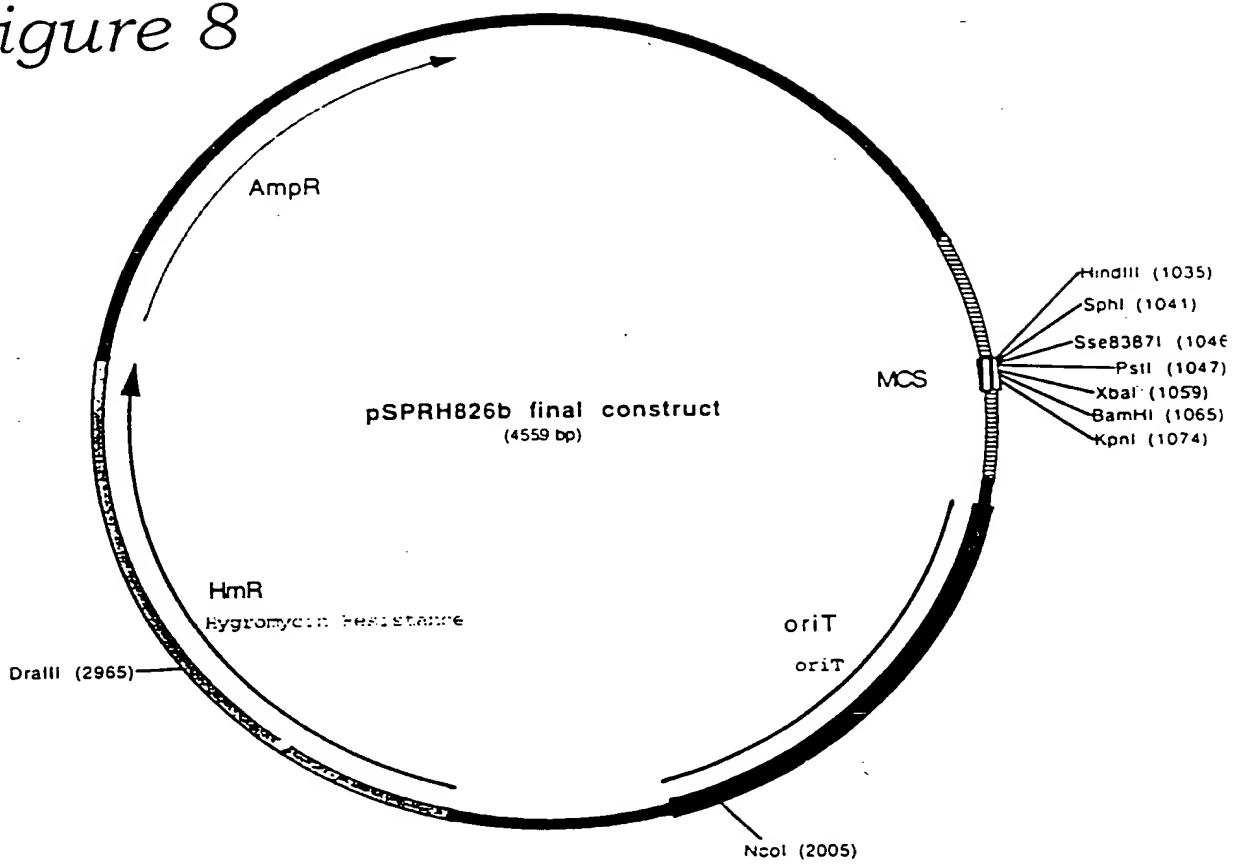Hygromycin Resistance

oriT
oriT

DraIII (2965)

NcoI (2005)

Figure 9

Analysis of *M. carbonacea* and *M. halophytica* pSPRH840 insertion site AttB/AttP region

A. Alignment of pMLP1 attP region with religation clone edge sequence

```
M.halophytica PstI relig-9   TGATCAACTCTAGGGCAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCCGA   60
M.carb PstI relig-1          TGATCAACTCTAGGGCAGGGGTAGGGGAAT-CNCTCCGGAGACGCCCGGAGCAATCCCGA   59
M.carb PstI relig-4          TGATCAACTCTAGGGCAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCCGA   60
pMLP1.inttCA.att region      TGATCAACTCTAGGGCAGGGGTAGGGGAATCCNCTCCGGAGACGCCCGGAGCAATCCCGA   60
Consensus                    TGATCAACTCTAGGGCAGGGGTAGGGGAATCCNCTCCGGAGACGCCCGGAGCAATCCCGA   60

M.halophytica PstI relig-9   CCATCACGGACGACCAACCACGCACGTCAGCTCCCTCTTCACCCCGTCACCAGGCCCCGGTA   120
M.carb PstI relig-1          CCATGACGACGACCAACCACCACGTCAGTCAGCTCCCTCTTCACCCCGTCACCAGGCCCCGGTA   119
M.carb PstI relig-4          CCATCACGGACGACCAACCACGCACGTCAGCTCCCTCTTCACCCCGTCACCAGGCCCCGGTA   120
pMLP1.inttCA.att region      CCATCACGGACGACCAACCACGCACGTCAGCTCCCTCTTCACCCCGTCACCAGGCCCCGGTA   120
Consensus                    CCATCACGGACGACCAACCACGCACGTCAGCTCCCTCTTCACCCCGTCACCAGGCCCCGGTA   120

M.halophytica PstI relig-9   CCGGTTCAATCCCATCAGTCACCCAGTTCACACGCCCAGGTCAGCGCCCGTTCTCACC-G   179
M.carb PstI relig-1          CCGGTTCAATTCCCATCAGTCACCC----GT-ACACCGAAGGGCCCCCTCCAC-TCCGAGGGG   174
M.carb PstI relig-4          CCGGTTCAATTCCCATCAGTCACCC----GT-ACACCGAAGGGCCCCCTCCAC-TCCGAGGGG   175
pMLP1.inttCA.att region      CCGGTTCAATTCCCATCAGTCACCC----C---GCCAAGTGGATCTACTCCACACAGCAGATCAG   175
Consensus                    CCGGTTCAATTCCCATCAGTCACCCCAGCGRARSANSHRGRYCNVSKCCRSWKCDSABSRG   180

M.halophytica PstI relig-9   CCCCT-CACCCATTTTCACGGG------   200
M.carb PstI relig-1          CCTTCGCCGT-TCCTCAGGGTTCGG-    200
M.carb PstI relig-4          CCTTCGCCGT-TCCTCAGGGGTTCGG-   200
pMLP1.inttCA.att region      CCCCCTCCG----AAGACGGGCCCTGAT   200
Consensus                    CCCYCKVCGYATNMSAGGCKKCSYGAT   209
```

B.   pMLP1 attP region

```
1    TGATCAACTCTAGGGCAGGGGTAGGGGAATCCACTCCGGAGACGCCCGGAGCAATCCCGACCATCACGGACGACCAACCACGCACGTCAGCGTCCCT

94   GTTGACCCCCTGACCAGGGCCCCGGTACGGGTTCAATTCCCATCAGTCACCGGCCAAGTGGATCTACTCCACACAGCAGATC
```

Insertion juncture

```
174  AGGGCCCCTCCGGAAGAGGGGGCCTGATGCCGTCATAGGGGACAGGTAGGGAACTCAA
```

Figure 10

Cloning scheme to test
potential resistance genes

```
   1 GGTACCCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCGAGAGGAACACCCCCCGGTAGTCCGGGTAGACGGTGGGCGCGAAGGCGTAC
  93 GCGCCTTCGACGGTCAGCGGGCGGGCGGACACCGGCGGGTCAGCTCGTCACGTGTACGCGGGGGACGTACAGGATCCACTGTCCGCCAGCC
                                        <  •  S   T   V   H   V   R   P   V   Y   L   I   W   Q   G   G   A
 184 CGGCGGAACTCCTGCTCCTTCGCCATGATCTCGTCGGCGTGGTTCCAGGCGAAGAGCAGCGCGTAGTCCACCGCGTCGGGCGTGAACGCGTC
       <R   R   F   E   Q   E   K   A   M   I   E   D   A   H   N   W   A   F   L   L   A   Y   D   V   A   D   P   T   F   A   D
 276 CGGGGTGCGCACCGGGATGTGCGTGCCGGGGGTGAGCCGGCCCTGCTTGGCCGGCGTCGTGTCGCACACCAGGAGACCAGGTCCGGACCGA
       <  P   T   R   V   P   I   H   T   G   P   T   L   R   G   Q   K   A   P   T   T   D   C   V   W   S   V   L   D   P   G   I
 368 TGCCGCAGAAGTTCGTCACGGTGGCGCTCTTCGCCGTCGCGCCGTACGCCACCACCCGCTTGCCCTCGGCCTTGAGCGAGTTCAGCAGGGCG
       <  G   C   F   N   T   V   T   A   S   K   A   T   A   G   Y   A   V   V   R   K   G   E   A   K   L   S   N   L   L   A
 460 AGCAGGTCGGTGCGGATGCCCTCGACGTCGGCGGCGAACCTGTCGAGCCGGCTGCGGTCGGCGACCCCTCGGGCGTCCTCCTCGCCGATCAG
       <L   D   T   R   I   G   E   V   D   A   A   F   R   D   L   R   S   R   D   A   V   G   R   A   D   E   E   G   I   L
 552 CGCCGGCCACCCGCTCGGCCGGCTGCCGCGCGCCGGCACGGCCGATGGTGTAGCGGACCTCCCCACCGTGCACCGGAAGGCGTTCCACGTCGA
       <  A   A   V   R   E   A   P   Q   R   A   G   A   R   A   I   T   Y   R   V   E   G   G   H   V   P   L   R   E   V   D   V
 644 CGAGCGCGAAGCCGAAGCGGGCCGCCAGCGCCTGCACCGACCGCGCCGAGAAGAAGAAGAAATGCTCGTCGTAGATCTGGTCGAAGGACGTC
       <  L   A   F   G   F   R   A   A   L   A   Q   V   S   R   A   S   F   F   F   F   H   E   D   Y   I   Q   D   F   S   T
 736 TTGTCCAGGATGTCCCCGAGGTACGGGTCCTCGAAGACGAAGACCCCGTCCGGTGCCAGCAGCGCGTCAACGCCCCGGAGGATGGAGTCGAG
       <K   D   L   I   D   G   L   Y   P   D   E   F   V   F   V   G   D   P   A   L   L   A   D   V   G   R   L   I   S   D   L
 828 GTAGGGGATGTGGCAGATGGTGTTGGCCGCGAAGATCACATCGGCGGGGCCGTCGGTCTCCCTGACCCGGCGGGCGGTGGACTCCTCGAAGA
       <  Y   P   I   H   C   I   T   N   A   A   F   I   V   D   A   P   G   D   T   E   R   R   R   A   T   S   E   E   F   F
 920 ACTCGGTGACCACCGCACCCCGTGCCCACGGGCCACATCGGCCACCCCACCCGACGGCTCGAAGCCCAGGTGCCGCACTCCCGCCTCGTGG
       <  E   T   V   V   R   V   G   H   G   R   A   V   D   A   V   G   G   S   P   E   F   G   L   H   R   V   G   A   E   H
1012 ACGGTACGCAGCATCACCCCGTCGTTGCAGCCGATCTCCACCACGAACGGGTCCGGGCCGGTGGCCTCGTGCTCCAGCAGGTGCCGCGCGGT
       <V   T   R   L   M   V   G   D   N   C   G   I   E   V   V   F   P   D   P   G   T   A   E   H   E   L   L   H   R   A   T
1104 GTCGGCGAAGTGCTTCTGCATCACGGAGGAGCCCGACGAGTGGTACGGGTAGTCCTGGTGGAACATCTCCTCCCGGGGCACCTCCTCCATGA
       <  D   A   F   H   K   Q   M   V   S   S   G   S   S   H   Y   P   Y   D   Q   H   F   M   E   E   R   P   V   E   E   M   L
1196 GCTGCACCATCGTGCAGCCCGCGCAGACCCCCACCGCCAGGTGGAAGAAGAACTCGTCCGCGAGCTGGTCCTCGGTGAGGAACCGGTCGGAG
       <  Q   V   M   T   C   G   A   C   V   G   V   A   L   H   F   F   E   D   A   L   Q   D   E   T   L   F   R   D   S
1288 AGCGGCTGCCGGACCCAGGTCGAGGAACTGGGCGGTGGTGCCGCCACGCCCAGGTGCCGCGCGGGGCGTGCCGTCGGCTGAATCGGT
       <L   P   Q   R   G   L   D   L   F   Q   A   T   T   G   G   C   A   R   C   T   G   R   R   P   T   G   D   A   S   D   T
1380 CATCGCATTCCTTCCATGGATACCCCTGCCTCAGGCAGGGCGGATGTCAACGACGTCTCCTTGTCGGGATGGGTCGTCCAGCTCTCGGC
       <  M
1469 TGCGGCGTGCCGGCCGGCGACTCAGAGCGCCGCGAGCACGTCGCGCAGCGCGTCGATCACCCGGTCCTGCGTCTCCGGCGGCAGCGAGGGA
                                  <  •  L   A   A   L   V   D   R   L   A   D   I   V   R   D   Q   T   E   P   P   L   S   P
1560 TACATGGGGAGGGAGAAGATCTCGCCGGCCAACCGTTCCGTGGTGGGGAGGGAGCCGGTCTGGTAGCCGAGCTTGGCGAAGCCGGTCATGGT
       <Y   M   P   L   S   F   I   E   G   A   L   R   E   T   T   P   L   S   G   T   Q   Y   G   L   K   A   F   G   T   M   T
1652 GTGCACCGGCCAGGGGTAGCTGATGTTGAGCGCGATGTCCCGCGCCGCCAACTGTTCGAGGATGCGGTCGCGGGCGGGGTGGCGGACCACGT
       <  H   V   P   W   P   Y   S   I   N   L   A   I   D   R   A   A   L   Q   E   L   I   R   D   R   A   P   H   R   V   V   Y
1744 AGACGTACCAGACGTGTTCGTTGTCGGTCGCCGTCACCGGCAGGGTCAGGCCGACCTGGTCGGCGGATGTCGGCCAGGCCCTCCTCGTAGCGC
       <  V   Y   W   V   H   E   N   D   T   A   T   V   T   R   L   T   G   V   Q   D   A   I   D   A   L   G   E   E   Y   R
1836 CGGGCCACGGCGCGGCGCCCGGCGATGTAGTCGTCGAGCCGGCACAGCTTGCGGCGCAGGATCTCGGCCTGCACCTCGTCGAGGCGGCAGTT
       <R   A   V   A   R   R   G   A   I   Y   D   D   L   R   C   L   K   R   R   L   I   E   A   Q   V   E   D   L   R   C   N
1928 GTGCCCCGGCGTCTCGACGACGTAGTAGACCTGTTCCATGCCGTAGTAGCGCAGCCGCCGCAGCCGCTCGTCGATCACGGCGTCCGCGGTGA
       <  H   G   P   T   E   V   V   Y   Y   V   Q   E   M   G   Y   Y   R   L   R   R   R   L   R   E   D   I   V   A   D   A   T   V
2020 CCACGCCGCCGCCGTCGCCGTACGCGCCCAGCACCTTCGTCGGATAGAACGAGAAGGCAGCGGCGTCGCCCATCGTGCCGGCCAGCCGTCCG
       <  V   G   G   G   D   G   Y   A   G   L   V   K   T   P   Y   F   S   F   A   A   A   D   G   M   T   G   A   L   R   G
2112 CCCCGACGCGCGCCGTGCGACTGCGCGCAGTCCTCCAGGACCTTGAGGCCGTGTTCCCGGGCCACCCGCAGCACCGGGTCCATGTCGACGCA
       <G   R   R   A   G   H   S   Q   A   C   D   E   L   V   K   L   G   H   E   R   A   V   R   L   V   P   D   M   D   V   C
2204 CTGGCCGTAGAGGTGCACCGGCAGCAGCGCCTTCGTCCGGGGGGTGACCGCCTCGGCCAGCAGCTCGGTGTCCATCAGGTAGTCGTCGGCGC
       <  Q   G   Y   L   H   V   P   L   L   A   K   T   R   P   T   V   A   E   A   L   L   E   T   D   M   L   Y   D   D   A   R
2296 GGACGTCCACGAAGACCGGCGTCGCGCCGACCGCGTCGATGGCGAGCACCGTCGGCGGCCGTGTTGGAGACGGTGATGACCTCGTCGCCC
       <  V   D   V   F   V   P   T   A   G   V   A   D   I   A   L   V   T   P   A   A   T   N   S   V   T   I   V   E   D   G
2388 GGCCCGACGTCGAGCGCCTGGAGTGCGAGCTTGATGGCGTTGGTGCCGTTGTCCACCGTGACGCAGTGCGGCATGTCGTGATAGGCGGCGAA
       <P   G   V   D   L   A   Q   L   A   L   K   I   A   N   T   G   N   D   V   T   V   C   H   P   M   D   H   Y   A   A   F
2480 CTCCTGCTCGAAGCCGCGCACGCTCGCGCCGAGGATGAGGTTCCCGGACTCGAAGACCGTCTGCACGGCGTCGAGGAGGTCGTCCCGTTCCT
       <  E   Q   E   F   G   R   V   S   A   G   L   I   L   N   G   S   E   F   V   T   Q   V   A   D   L   L   D   D   R   E   K
2572 TCTCGTACTCCGGCAGGTAGCCCCACACTCGGATGGTCATCTTCGCCCTTCTACGCCGAGGTCCGGGAGCGGAGCGCGCACGCTCAT
       <  E   Y   E   P   L   Y   G   W   V   R   I   T   M          <  •  A   S   T   R   S   R   L   A   R   V   S   M
2661 GTAGTCGTTGTCCCGGTCGAGTCCAAGTGCCTGACCGCTCAGGTAGTCGACGGCGTCCACGTAGCTGTAGGGCTGCATGAACCCGCCGGCCC
       <  Y   D   N   D   R   D   L   G   L   A   Q   G   S   L   Y   D   V   A   D   V   Y   S   Y   P   Q   M   F   G   G   A   R
2753 GCACGTCGCGATAGAGCCGGGAGAGTGGGTGCCGGCCGTGTAGGCGGCGCCGACCAGGCTGAGGCAGTCGTCCACCACCGCCGGGGCC
       <  V   D   R   Y   L   R   S   L   P   H   G   A   T   Y   A   L   G   G   V   L   S   L   C   D   D   V   A   P   A
2845 AGCTCGTTGACGGTCATCTTCGCGTACTGGAACGGGGTCATCATCCGTCGGCCGCGTTCGTCCGGGTCGCCGGACAGGTCGACCGACGCCGC
       <L   E   N   V   T   M   K   A   Y   Q   F   P   T   M   M   R   R   G   R   E   D   P   D   G   S   L   D   V   S   A   A
2937 GTCGGCGTTGGTCAACGCCGCGCCGACCGTGGTGCGTAGCGCGTAGAGCCGGGTGTCCAGCCCGGCGACCAGCGCCCGGGCACCGGCCCGTG
       <  D   A   N   T   L   A   A   G   V   T   T   R   L   A   Y   L   R   T   D   L   G   A   V   L   A   R   A   G   A   R   P
3029 GCTCGCCGCCGCGCCCCGCGCAGAAACCGACCGCGATGTCCCGGTCCCTGGGCGATGCCGGCGTAGATGCCGAGCATGTGATCGAGCTG
       <  E   G   G   R   G   A   C   F   G   V   A   I   D   R   A   A   Q   A   I   G   A   Y   I   G   L   M   T   I   S   S
3121 ACCGTCTGCCCGGCCAGCACGGCGTCCCGCCGGGCCCCGACCGGGCCGCGCTCCAGCAGCTCGTCGGCCCGGACCGGGCACCGGTCGAAGAC
       <V   T   Q   G   A   L   V   A   D   R   R   R   A   G   V   P   G   R   E   L   L   E   D   A   R   V   P   C   R   D   F   V
3213 CACCTCCAGCGTCCCCGAGGCACGCATTCCCAGGCCGTCCCAGTTGTCCAGCACCGTGAGCCCGGGGGCGTCGCGGTGCACGACCGGCACGG
       <  V   E   L   T   G   S   A   R   M   G   L   G   D   W   N   D   L   V   T   L   G   P   A   D   R   H   V   V   P   V   A
3305 CGAGGAACACCGAGCCGTCGTCGTCGCGCCGCTGGGCGTGCACGAAGAAGTGGGTCGCGATGGGCCGCCATGCTGACCAGCACCTTGCGGCCC
       <  L   F   V   S   G   D   D   D   R   R   Q   A   H   V   F   F   H   T   A   I   P   A   M   S   V   L   V   K   R   G
3397 GACAGCAGCCAGCCGCCGGCGCCGTCGGAATGCAGCTCGGTGACCACGCCGGGGGCGTCCTTGAGCGCGCCGCAGACGGCGGCCTCGCCCTC
       <S   L   L   W   G   G   A   G   D   S   H   L   E   T   V   V   G   P   A   D   K   L   A   G   C   V   A   A   E   G   E
3489 CGCCATCGCCGCCAGCAGCCGCTCCAGCACTCGCGGCGACCGGCGGCCGTGCTGCCACTCGTAGGTGAGGGTGAGGCCCCGGCTGAGCT
       <  A   M   A   R   L   L   R   E   A   M   A   R   V   P   T   G   H   Q   W   E   Y   T   L   T   L   G   R   S   L   Q
3581 GCACGTGCCAGGCCAGCGCGGTGGACGCGTCGGCCTCGGCCAGCCGCATCAGCGCGGTCGCCACGTCGTACAGCCGGGTCAACCCCAGGCCG
       <  V   H   W   A   L   A   T   S   A   D   A   E   A   L   R   M   L   A   T   A   V   D   Y   L   R   T   L   G   L   G
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Figure 11A

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3673 CCCAGCTCGGCGGGAACGGTGGCGCCCATCAACCCGAGCTTCGCGAACTGCTCGAACGCCTCCACCGGGAAGGTGCCGGTGCGGTCCCGGTC
      <G L E A P V T A G M L G L K A F Q E F A E V P F T G T R D R D
3765 GGCGGCCTCCGCACTGATTCTCGGGATCACGCCGGCAAGCAGGTCGACCACCGTGCGCCCCGCCGGCGTGAGCGGCGCGCGAAGATCCGCCG
      <A A E A S I R P I V G A L L D V V T R G A P T L P A R L D A A
3857 CCACCCATCTCTCCTCGGTCAGATTAGACATCGCCTGCTTCCGTTCGCGCTGTGCCGAACCTGTCGCTATCAGGGTGCGCGGCGATCACC
      < V
3947 AATTGCTGGCTGATTGTCCACCGACGATGCTCGACAGGGATACCCAGAATAGGCGGCAACGGCTTGGCGAAACCCCTGTCGTGCGCCGGAGT
4039 TCGCCAAGTCTAGTTGGATCACTCGAGCTTCCCCCGCAGAAGCCGTGAACCATGGGCCAGCGGTTGACGTCGCTATATATTCGGCCGACACG
4131 TGCGGAGGACTCGTGAAGATACTGTTCATCGCAGGACCGACGAAGTCCAGCCTATTCGGCCTGGCCCCACTGGCAATCGCCGCCCGGATG
      > V K I L F I A G P T K S S L F G L A P L A I A A R M
4221 AGCGGGCACGAGGTCGTGATGGCTTCCACGCAGGAGGTCGTACCGGCAGCGATGTCCGTCGGGCTGCCGGCCTTCCCGCTGGCGGCGCTGAC
      > S G H E V V M A S T Q E V V P A T M S V G L P A F P L A A L T
4313 CCTCGCCGAGCTCATGACCACCGACCGGGCCGGCGATCCGCTGCGCATCCCGGCCGAGGACGCCGCCTTCGTCCCCTTCGTCGGCCGGATGT
      > L A E L M T T D R A G D P L R I P A E D A A F V P F V G R M
4405 TCGGCCGGCTGGCGGCGATCAGCCTGGATCCGCTGCGCGACCTGGTCGGCGGGTGGCGGCCCGACCTGATCGTCGGCGGCCCGCACGCCTAC
      >F G R L A A I S L D P L R D L V G G W R P D L I V G G P H A Y
4497 GCCGCGCCGATCCTGGCCACCGAACTTGGGGTGCCCTGCGTGCGGCACCTGCTCACCGGCAACCCGGTGGACCGCGAGGGCACCCATCCGGG
      > A A P I L A T E L G V P C V R H L L T G N P V D R E G T H P G
4589 GGTCGACGAGGAGCTGCGGCCGGAGCTGGCCGCGCTCGGCCTGGCCCAGGTGCCGCCGTTCCACCTGGCCCTGGACATCTTCCCGGCCAGCA
      > V D E E L R P E L A A L G L A Q V P P F H L A L D I F P A S
4681 CCCGGACCGACGACGTCCCGCCGGCGCAGCCGGTGCGACCGCTGCGCTGGATTCCGACCAACCAGCAGCAGCCGGTGGCGCCGTGGATGCTC
      >T R I D D V P P A Q P V R P L R W I P T N Q Q Q P V A P W M L
4773 TCGCGCGGGCCGCGTCGCCGTGTCCTGGTCACCGCCGGCAGTCTGGTCACCACCACCCACAACTTCGACTTCCTCCACGGACTGGCCGGCAC
      > S R G P R R R V L V T A G S L V T T T H N F D F L H G L A G T
4865 CCTGGCCGAGCAGGACGTCGAGGTCGTGGTCGCGGCGCCGCCGGAGGTGGGTCGGGCCCTGCACGACGTGCCGGGTGTGCGGCACGCCGGCT
      > L A E Q D V E V V V A A P P E V G R A L H D V P G V R H A G
4957 GGCTCCCGCTGGACGTGGTGCTGCCCCACTGTGACCTGATCGTGCACCACTCCGGCACGATGACCGCGCTGACCGCCTTGAACGCGGGGGTG
      >W L P L D V V L P H C D L I V H H S G T M T A L T A L N A G V
5049 CCCCAGCTGATCGTGCCGCAGGAGAGCCGGTTCATCGAGTGGGCGCGCAACCTGTCGACCCTGGGCGTGGCGCAGACCCTCGCGCCGGGCGA
      > P Q L I V P Q E S R F I E W A R N L S T L G V A Q T L A P G E
5141 GGACACGCCGGAGGCCGTGGGCAAGGTCGCCCGCCTGCTGCTGGAGGATCCGGTCCACGCCACCAGCGCCGCCGCGATCGCCCGGGAGATCG
      > D T P E A V G K V A R L L L E D P V H A T S A A A I A R E I
5233 CCGAGATGCCCGGCCCCACGGAGGTCGTGGGCCAGCTCACCGAGTTCGCGACCCGGGGCCTGACATGCGCGTCCTCGTGACCGGCGGAGCC
      >A E M P G P T E V V G Q L T E F A T R G L T C A S S •
                                                          > V T G G A
5324 GGGTTCATCGGCTCCCACCTCACCGACGCGCTGCTCGAACGCGGCGACAGCGTCACCGTGCTCGACGACCTGTCCACCGGGCGGCCCGAGCG
      > G F I G S H L T D A L L E R G D S V T V L D D L S T G R P E R
5416 GCTGCCCGCCGGGGTGCCGCTGCACCACGGGTCGATCACCGACCGGGCGGGTTGACCCGGCTGGCCGAGCAGTGTCGCCCGGAGGTCATCT
      > L P A G V P L H H G S I T D R A G L T R L A E Q C R P E V I
5508 GCCACCTGGCCGCCCAGGCGGACGTGCGCAACTCGGTGGCCGACGCCACCTCGGACACCGGGGTCAACGTGGTCGGCACCGTCAACGTCCTG
      >C H L A A Q A D V R N S V A D A T S D T G V N V V G T V N V L
5600 GAGGCCGCCCGGGCCATCGACGCCCGGGTGGTCTTCGCCTCCAGCGGCGGCGCCCTCTACGGGGAGGTCGACGAGCTGCCCTCCCCCGAGGA
      > E A A R A I D A R V V F A S S G G A L Y G E V D E L P S P E D
5692 CGTCCGGCCGGCGCCGTGGGCGCCGTACGGGGCCGCCAAGTACTGCGCGGAGCAGTACCTGGCGCTCTACAACCGGCTCTACGGCTCGACCC
      > V R P A P W A P Y G A A K Y C A E Q Y L A L Y N R L Y G S T
5784 ACGCGGCGCTGCGGCTCGGCAACGTGTACGGGGCCACGCCAGGACCCGACCGGCGAGGCCGGGGTCGTCTCGATCTTCTGCGGCTGCCTGGTG
      >H A A L R L G N V Y G P R Q D P T G E A G V V S I F C G C L V
5876 GCCGGGCGCCGGCCGACGGTGTTCGGCGACGGCGAGCAGACCCGGGACTACATCTACGTGGCCGACGTGGTGGAGGCGTTCCTGCTCGCGGT
      >A G R R P T V F G D G E Q T R D Y I Y V A D V V E A F L L A V
5968 CGGGCACGGTGGCCCCGGCCTGTGGAACATCGGCACCGGGACCTCCACCAGCATCCGCAAACTACTGGACCTGGTCGGCCGCACCGCCGGGC
      > G H G G P G L W N I G T G T S T S I R K L L D L V G R T A G
6060 GCGTCCCGGACCCCCGCTTCGAGCCACCCCGCCTGGGCGAGCTGAAGCACTCCGCGCTGGAGGTGACCCGCGCGGCCCGGGAGCTGCGCTGG
      >R V P D P R F E P P R L G E L K H S A L E V T R A A R E L R W
6152 GCGGCCCGAACGAGGCTCGCCGACGGCATCGCGAAGGTCTACAAGTGGGTCGAGGCGGACGAACCGGTCCGGGGGGAGCGATGACCCGCG
                                                                          > M T R
      >A A R T R L A D G I A K V Y K W V E A D E P V R G E R •
6242 AGGGGTCAACGCCGCCGGTTAGGGTCGCCACCATCACGGTCGGCACCAACGAGATCCGTTGGCTGGACCGCGCGCTCGGCTCGCTGCTCGCC
      >E G S T P P V R V A T I T V G T N E I R W L D R A L G S L L A
6334 AGCGACACGACCGGCTTCGAGCTGACGGTCTTCTACGTGGACAACGCCTCGGCCGACGGCAGCGTGGCGCACGTCATGTCGGCGTTTCCCGG
      >S D T T G F E L T V F Y V D N A S A D G S V A H V M S A F P G
6426 CGTCCGGGTCATCCGAAACCCCCGCAATCTCGGCTTCACCGGCGCGAACAACGTCGGCATGCGGGCGGCCCTGGCGGAGGGCTTCGACCACA
      > V R V I R N P R N L G F T G A N N V G M R A A L A E G F D H
6518 TCTTCCTGGTCAACCCGGACACCTGGACACCGCCGGGGCTGGTCCGCGGGCTGGTCGAGTTCGCGCAGCGGTGGCCGCAGTACGGCGTCATC
      >I F L V N P D T W T P P G L V R G L V E F A Q R W P Q Y G V I
6610 GGCCCCGTTGCAGTACCGCTACGACCCGGCGTCGACCGAGTTGACCGACTTCAACGACTGGACGCAGGTCGCCCTCTACCTGGGCGAGCAGCA
      >G P L Q Y R Y D P A S T E L T D F N D W T Q V A L Y L G E Q H
6702 CACCTTCGCCGGCGACCTGCTGGATCATCCCTCGCACGTCACCGCGACGGTCCGCGACCGCGCGCCGCGCACCCTGGAGCACGCGTACGTGC
      > T F A G D L L D H P S H V T A T V R D R A P R T L E H A Y V
6794 AGGGCTCGGCGCTGTTCGTCCGGGCCGCCGTGCTACGCGAGGTCGGCCTGCTCGACGAGGTGTTCCACACCTACTACGAGGAGGTCGACCTG
      >Q G S A L F V R A A V L R E V G L L D E V F H T Y Y E E V D L
6886 TGCCGGCGGGCCCGGTGGGCGGGGCTGGCGGGTGGCGCTCCTACTCGACCTCGGCATCCAGCACAAAGGCGGCGGTGGCGGCACCGCGAGCGC
      > C R R A R W A G W R V A L L L D L G I Q H K G G G T A A S A
6978 GTACAGCCGGATACACATGCGCCGCAACCGCTACTACTATCTGCTGACCGATGTGGACTGGCCCCCGGCCAAGGCCGCCCGGCTCGCCGCCC
      > Y S R I H M R R N R Y Y Y L L T D V D W P P A K A A R L A A
7070 GCTGGCTGTTCTCCGACGTCCGTGGGCGGGGGCGTGACGGGTCGGACGAGCGGGGCGTCGGGGCGCGGGAGACCTTCGTGGCGCTCGGGTGG
      >R W L F S D V R G R G V T G R T S A G V G A R E T F V A L G W
7162 CTGGCCCGCCAGGCCCCCGGTGATCCGGGAACGTCGTCGGCGGCACCGGCTGCTGCGGGCACGAGGGACGTGGACCGCGCGCCCGAGAGCG
      >L A R Q A P V I R E R R R R H R L L R A R G T G V D R A R E R
```
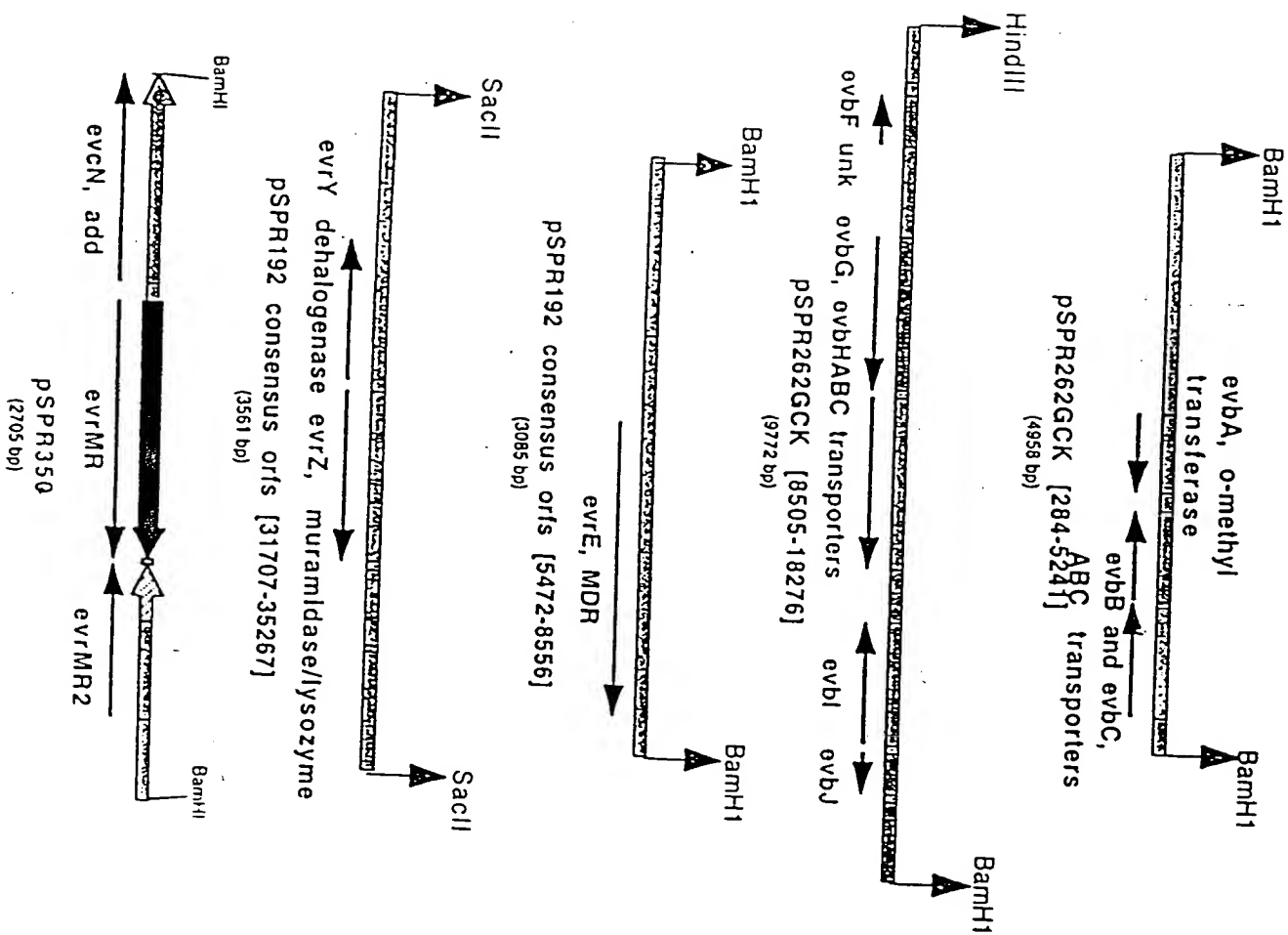
Figure 11B

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7254 GAAGGAAACCGTGCGGGGATGAGCAGGCCACGGATTCTCGTCGCGGGCAACTTCCACTGGCAGGCCGGGTTCAGCCAGACCGTCGCCGCGT
       >  K   E   T   V   R   G   •
                              >M   S   R   P   R   I   L   V   A   G   N   F   H   W   Q   A   G   F   S   Q   T   V   A   A
7345 ACGTGCGGGCGGCCCGGGAGGCCGACTGCGAGGTGCGGCTCTGCGGGCCCGCTGTCCCGGGTCGACGCCGAGACGGCCCGGCACCTGCCGGTC
     >Y   V   R   A   A   R   E   A   D   C   E   V   R   L   C   G   P   L   S   R   V   D   A   E   T   A   R   H   L   P   V
7437 GAGCCGGACCTCCGCTGGGGCACCCACCTGGTGATCATGTTCGAGGCCAAGCAGTTCCTCACCGAGGCGCAACTGGACCTCGTCGAGGCGTT
     >E   P   D   L   R   W   G   T   H   L   V   I   M   F   E   A   K   Q   F   L   T   E   A   Q   L   D   L   V   E   A   F
7529 CCCCCCGACAGCGCCGGGCCATCGTCGACTTCGACGGGCACTGGGGTGCCGAGGAGGGCGGGGACGGCGACAGCGCGTCGGGCCGGTACTCCG
     >  P   R   Q   R   R   A   I   V   D   F   D   G   H   W   G   A   E   E   G   G   D   G   D   S   A   S   G   R   Y   S
7621 CGGAGAGTTGGCGGCGGTTGTACTCGACCCTGAGCGACCTGATCCTGCAACCCCGGCTGGGTCCGCTCCCGGCCGGCGCCCGGTTCTTCAAG
     >A   E   S   W   R   R   L   Y   S   T   L   S   D   L   I   L   Q   P   R   L   G   P   L   P   A   G   A   R   F   F   K
7713 TGCTTCGGCCTGGCAGCGCCGGTGCGGCACCCGCTGGAACTGGGCACCGGCGCGCAGTCGCGCCCGTACGACCTCCAGTACATCGGCAGCAA
     >C   F   G   L   A   A   P   V   R   H   P   L   E   L   G   T   G   A   Q   S   R   P   Y   D   L   Q   Y   I   G   S   N
7805 CTGGTGGCGGTGGGAGCCGATGACCGAGATGGTCGAGGCCGCGGCGGCGGCCCGGCCGCCGCTGCGCCGGCTGCGGGTGTGCGGACGCTGGT
     >  W   W   R   W   E   P   M   T   E   M   V   E   A   A   A   A   A   R   P   P   L   R   R   L   R   V   C   G   R   W
7897 GGGACGGCGGCAGTTGCGCGGGCTTCGAGGAGGCGACGCTCAGCGAGCCGGGCTGGCTGCGGGGCCGCGGCGTCGAGGTGCATCCGCCCGTG
     >W   D   G   G   S   C   A   G   F   E   E   A   T   L   S   E   P   G   W   L   R   A   R   G   V   E   V   H   P   P   V
7989 CCGTTCGGCCACGTGGTCGAGCAGATGGGCCGGTCGCTGATCTCACCGGTCCTGGTGCGGCCGCTGGTCACCAGCACCGGCCTGTTGACCCC
     >  P   F   G   H   V   V   E   Q   M   G   R   S   L   I   S   P   V   L   V   R   P   L   V   T   S   T   G   L   L   T   P
8081 CCGGATGTTCGAGACGCTGGCCTCGGGCAGCCTGCCCGTGCTCCCGGTCGCCGCGAAGTTCCTCGCGCCGGTCTACGGCGACGAGGCGGAAC
     >  R   M   F   E   T   L   A   S   G   S   L   P   V   L   P   V   A   A   K   F   L   A   P   V   Y   G   D   E   A   E
8173 ACCTGATGCTCGGCGACGACCCGGCCGGAACGCTGAGCCGGCTCTCGGCCGAGCACGAACGGTACGGACGACTGGTCGGTGAGATTCAGGAC
     >H   L   M   L   G   D   D   P   A   G   T   L   S   R   L   S   A   E   H   E   R   Y   G   R   L   V   G   E   I   Q   D
8265 CGGCTCCGCGTCGAGTACGGCTACCCTCGCGTCCTGCGGGACCTGCTCGATCTGCTGGCCTGAGGAATGAGGAGCAGATGACCCCCCTG
                                                                                       >M   T   P   L
       >  R   L   R   V   E   Y   G   Y   P   R   V   L   R   D   L   L   D   L   L   A   •
8354 CGGATCGCGATGGTCAACATACCGTTCCGGTTGCGGAGCGACGAGCGGCAGTGGATCACGGTCCCGCCGCAGGGGTACGGCGGGATCCAGTG
     >  R   I   A   M   V   N   I   P   F   R   L   P   S   D   E   R   Q   W   I   T   V   P   P   Q   G   Y   G   G   I   Q   W
8446 GATCGTGGCCAACAAGATCAAGGGCCTGCTCGAACTCGGGCACGAGGTGTTCCTGCTCGGTGCCCCGGGCAGTCCGCGTACGCATCCACGCC
     >  I   V   A   N   K   I   K   G   L   L   E   L   G   H   E   V   F   L   L   G   A   P   G   S   P   R   T   H   P   R
8538 TGACCGTGGTGCCGGCGGGCGAGCCCGAGGACATCCGGGCATGGTTGAAGTCCGCTCCGGTGGACGTCGTCAACGACTACAGCTGCGGCAAG
     >L   T   V   V   P   A   G   E   P   E   D   I   R   A   W   L   K   S   A   P   V   D   V   V   N   D   Y   S   C   G   K
8630 GTGGATCCGATCGAGCTGCCCCCGGGGGTCGGCCTGGTGGCCTCGCACCACATGACCACCCGCCCGTCCTATCCGGCCGGCTGCGTGTACGC
     >  V   D   P   I   E   L   P   P   G   V   G   L   V   A   S   H   H   M   T   T   R   P   S   Y   P   A   G   C   V   Y   A
8722 CTCGAAGGCGCAGCGGGAGCAGTGCGGCGGCGGCGCGGACGCCCCGGTCATCCCGATCGGGGTGGATCCGTCGCTCTACCGCCCCGGCGACC
     >  S   K   A   Q   R   E   Q   C   G   G   G   A   D   A   P   V   I   P   I   G   V   D   P   S   L   Y   R   P   G   D
8814 GCAAGGACGACTTCCTGCTCTTCATGGGCCGGATCTCCCCGTTCAAGGGCGCGCTGGAGGCGGCCGCGTTCGCCCGGGCCGCCGGCCGCCGG
     >R   K   D   D   F   L   L   F   M   G   R   I   S   P   F   K   G   A   L   E   A   A   A   F   A   R   A   A   G   R   R
8906 CTACTGATGGCCGGTCCGGCCTGGGAGCCGGAGTACCTCGACCGGATCATGGGCGAGTACGGCGACCACGTCACCCTCGTCGGCGAGGTGGG
     >L   L   M   A   G   P   A   W   E   P   E   Y   L   D   R   I   M   G   E   Y   G   D   H   V   T   L   V   G   E   V   G
8998 GGGTCAGGAACGTATGGACCTGCTCGCCACGGCGGCTGCCATCCTGGTGCTCTCCCAGCCGGTGCCCGGCCCGTGGGGCGGCACGTGGTGCG
     >  G   Q   E   R   M   D   L   L   A   T   A   A   A   I   L   V   L   S   Q   P   V   P   G   P   W   G   G   T   W   C
9090 AGCCGGGTGCGACCGTGGTGTCCGAGGCGGCGGCCAGCGGCACCCCGGTGGTCGGCACGAGCAACGGCTGCCTGGCGGGAGATCGTGCCGGCC
     >E   P   G   A   T   V   V   S   E   A   A   A   S   G   T   P   V   V   G   T   S   N   G   C   L   A   E   I   V   P   A
9182 GTCGGCGAGGTGGTGGGCTTCGGCACCGGCTTCGACGAGCGGGAGGCCCGAGCGGTGCTGTCCCGACTGCCGTCGCCCGCCCAGGCGCGGAA
     >  V   G   E   V   V   G   F   G   T   G   F   D   E   R   E   A   R   A   V   L   S   R   L   P   S   P   A   Q   A   R   K
9274 GGCCGCGATCCGGTGCTGGGGGGCACGTGGAGATCGCCCGGCGCTACGAGGCGGTGTACCGCGACGTGCTGGCCGGCGCGCTGGTCCTGA
     >  A   A   I   R   C   W   G   H   V   E   I   A   R   R   Y   E   A   V   Y   R   D   V   L   A   G   A   R   W   •
9365 GCCGGCCCGGGCGGCGGCTACGGTCGCGACCGCAGGTCGCGGCTCGGGCGTCGGTCACCTCGACCGGCTGGCTCATGAACACCAGGACGTACGCGCGG
9457 GCCAGGTCAGCTCCGGTCGTCGCAGCCAGGTCGCGGCTCGGGCGTCGGTCACCTCGACCGGCTGGCTCATGAACACCAGGACGTACGCGCGG
     <   •   S   R   D   H   L   W   P   R   P   E   P   D   T   V   E   V   P   Q   S   M   F   V   L   V   Y   A   R
9548 CGCGGCTGGTCCGTCTCGTTCGGGCCGGCGTAGTGCGGCGCACGGAAGTCGTGCATGACCGCCTCGCCCGGCCGCAGCGGGCAGGCGACGCT
     <R   P   Q   D   T   E   N   P   G   A   Y   H   P   A   R   F   D   H   M   V   A   E   G   P   R   L   P   C   A   V   S
9640 GTCCGTGTCGTCGACCTCCGTCCGTCATCAGACCTTCGATGCGGTCGTCGTGGTTGATGTGATGGTGCGGGAGCACCCCGCCCCGGTGCAGGC
     <D   T   D   D   V   E   D   T   M   L   G   E   I   R   D   D   H   I   H   H   H   P   L   V   G   G   R   H   L   G
9732 CCGGCAGGTACTGGAGACAGCCGCTGGACACCGTCGCCTCGTCGAGCGGGGTCCAGATGCTCAGGCCGCGACGGGACCAGCGCGGGTCCATG
     <  P   L   Y   Q   L   C   G   S   S   V   T   A   E   D   L   P   T   W   I   S   L   G   R   R   S   W   R   P   D   M
9824 TACGCCTCGTCCTGGTGCCACGGAGTGGGTGCGCCGTAGCGCGGCGGCTTGAGGATCGCGTGGCCGTAGAAGTCGAGTTCGTCCTCGGGGAT
     <Y   A   E   D   Q   H   W   P   T   P   A   G   Y   R   P   P   K   L   I   A   H   G   Y   F   D   L   E   D   E   P   I
9916 GTCGAGGAAAGCGGAGGCGATGGCCCGGCATCGCGCGAAGTGCCGGTCTCCACCAACTCCGGCAGGTATTTCTCCGGCCGGACGATCTGCG
     <D   L   F   A   S   A   I   A   R   C   R   A   F   H   A   T   E   V   L   E   P   L   Y   K   E   P   R   V   I   Q   P
10008 GGAGACGGGCAGGCGCGGCGTCGTCGCCACGGCCGGCGATGTCCCGGTAGTCGCCGGTGTCGGGCGACGCGTGATCGGCGAAGAGCCGGTCG
     <  L   R   A   P   A   A   D   D   G   R   G   A   I   D   R   Y   D   G   T   D   P   S   A   H   D   A   F   L   R   D
10100 TAGGCGGCCCGGAGCCAGGCGACCTCGGCGTCGTCGGCGAGCTGCGGGAGAGTCACGAAGCCATCGCGCCGGTAAGCCTCCAGCCGACGGTC
     <Y   A   A   R   L   W   A   V   E   A   D   D   A   L   Q   P   L   T   V   F   G   D   R   R   Y   A   E   L   R   R   D
10192 GACGACCTCCGCACCAACAGTCCCCACGGCCATTTGACCACCTCTCGGAATAGCCTGTCCGCGAATAAACCATACGGTAGGAACAGCGCG
     <  V   V   E   A   G   V   T   G   V   A   M
10282 GCGATACCGCTCCCGAGCGGGAAATAGGGATTCGACTAGTATTCGGTCCGCGCCGCTGCCAGAACGGCACGCGCTCTCGATTGTCCATTCAT
10374 CCCCGTGCGAGACTCGCCTCGATGTCCTCGATGTCGGTGGGGGGTTTGGGATGACCGGGCACAGCGCCGTCGCGCTGGACGTCGGCGGGGT
                                                             >M   T   G   H   S   A   V   A   L   D   V   G   G   V
10465 CGTCTACTACGACGAGCCGTTCGAGCTGGCCTGGCTCCAGGACACCTTCGACCGGCTCCAGGCCACCGACCCGACGCTCGACCTGCGTGCGT
     >  V   Y   Y   D   E   P   F   E   L   A   W   L   Q   D   T   F   D   R   L   Q   A   T   D   P   T   L   D   L   R   A
10557 TTCTGGAGCACGTCGAGCGGTTCTACCACTACGGCGAGGGCGACCCAACCGGCCGGACCTGGCTCCACTCGGAGGCCGCCGCGCTGAGCTGG
     >F   L   E   H   V   E   R   F   Y   H   Y   G   E   G   D   P   T   G   R   T   W   L   H   S   E   A   A   A   L   S   W
10649 TCGCGGGTCCAGTCCTGGGGCGAGCTGGCCCAGGAGATTCCCGGTGCCGTTCGCCGGGTCACCAGGCTGGCCAGGGAACTACCCGTCGT
     >S   R   V   R   Q   S   W   G   E   L   A   Q   E   I   P   G   A   V   R   A   V   T   R   L   A   R   E   L   P   V   V
10741 GATCGTCGCCAACCAGCCCCCCGAGTGCGCGGACGTACTGGCCCGGTGGCAGGTCAGCCAGGTCTGCCGGGAGGTGCTCCTCGACTCCCTCG
     >  I   V   A   N   Q   P   P   E   C   A   D   V   L   A   R   W   Q   V   S   Q   V   C   R   E   V   L   L   D   S   L
```

Figure 11C

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10833 TCGGGGTGGCCAAGCCCGACCCGGCCCTGCTCGGGCTCGCCCTGCGGCGGCTGGCGATCCCGCCCGCCGAGTTGCTGGTGGTGGGCAACCGG
         >V  G  V  A  K  P  D  P  A  L  L  G  L  A  L  R  R  L  A  I  P  P  A  E  L  L  V  V  G  N  R
10925 ACGGATCACGACGTCCTGCCCGCGCTCGGGCTCGGTTGCCCGGTGGCGTTCGTGCTGCCCGATCCGGCGTACCGCCGGCCGCCGGGCGTCCA
         > T  D  H  D  V  L  P  A  L  G  L  G  C  P  V  A  F  V  L  P  D  P  A  Y  R  R  P  P  G  V  H
11017 TCCGGACCTGGTCCGGGTCTACACGGAGCTGAGGGCGTTCCGCACCGGCTCCCCGCCCGCGGACGCCCGGGTCACCACCGTGGCGTCCCTGG
         >  P  D  L  V  R  V  Y  T  E  L  R  A  F  R  T  G  S  P  P  A  D  A  R  V  T  T  V  A  S  L
11109 CGGCCCTGGCCGACTCTCCCCTGACGAGTGCCACCCCGCGTTCGAACGCCGGCACCGGCGGACTTTGACGAAGGAGTGCAGTTGCGACGCC
         >A  A  L  A  D  S  P  L  T  S  A  T  P  R  S  N  A  G  T  G  G  L  •
11200 CCGCAGCGGTGGTCGGCGCCACCGGCTTCATCGGCTCACGCCTCGTCTCCCGCCTGGCCGAGGCCGGGCATCCGGTGGCGCGCTTCAGCCG
11291 TGCCGCCCCACCCGTCGTCGACGGCCGGCCCGCGCCGGGGCTCCGCGAGGCGGCAGGTCGTCTACTTCCTCGCCGCCCGGCTGAGCCCGGCGC
11383 TGGCGGAGCAGCAACCGGAACGGGTCGTCCGGGAACGCGAGTTGTTGCTGGACGTGCTAAGTCGCTGGCGGGGGTGGACCACCGGCCGGTG
11475 TTCGTCCTGGCCAGCTCGGGCGGGGCGGTGTACACGCCGACGGTGTGGCCGCCCTACCACGAGCGGTCGGCCACCGGGCCCGCCTCGGCGTA
11567 CGGCCGGGCGAAGCTGCGGCTGGAACAGGAGCTGCTGCGCCACACCGACCGGGTGCAGCCGGTGGTGACCCGGCTGAGCAACGTCTACGGTC
11659 CGGGGCAGCGGCCGACCCCCGGGTACGGTGTCCTGTCACACTGGCTGGAGGCCACCGTGCGCGGAGAGCCGATCCGGCTCTTCGGCGATCCG
11751 GCCGTGGTGCGGGACTACGTACACGTCGACGACGTCACCGCGATCATGGAGGTCATCGCGCAGCGGGCCGGTGACGGCGACCGGGACCGGCT
11843 GCCCACGGTCGTGAACGTCGGCTCGGGCCTGCCCACCTCCCTCGCCGAGTTGCTCCAGACGATGTCCACGGTGGCCGGTCGTGAGCTGGAGG
11935 TCATCCGGGACGTCCGCCGGCAGTTCGACCATCGGGGCAACTGGCTCGACACCACCCTCGCCCGGGAGACCCTGGGCTGGCAGGCGCGGATC
12027 AGCCTCCCCGACGGCGTCCGCCAGTGCTGGGAGGCCGTCCTCACCCGGGCGGGCGGCCCGGGGGGTTCCCCGGCCCGACCGTCAGCCCGGC
         > S  L  P  D  G  V  R  Q  C  W  E  A  V  L  T  R  A  G  G  P  G  G  S  P  A  R  P  S  A  R
                                                                              <  •  G  P
12118 TCGGGAGAGCGTCTCGGGGGCGGGAACCGCCGCAACCGCGCCCTTCGCAGCAGTTCGTGGCTCAACCCGGCGGCGGTCGCCGCGGTGTAGCC
         >L  G  R  A  S  R  G  R  E  P  P  Q  P  R  P  S  Q  Q  F  V  A  Q  P  G  G  G  R  R  G  V  A
         <E  P  S  R  R  P  P  P  P  F  R  R  R  L  R  A  R  R  L  L  E  H  S  L  G  A  A  T  A  A  T  Y  G
                                                                                      junction marker
12210 GAGGGCCAGTGGCAGGGCGAGCCGGGATTCCGGGGCCGTACGGTGCCGGTCCCATTCCTTGCGCAGGCCGGCCCGTGCCTGGTTCCGTCCGG
         >  E  G  Q  W  Q  G  E  P  G  F  R  G  R  T  V  P  V  P  F  L  A  Q  A  G  P  C  L  V  P  S  G
         <  L  A  L  A  L  R  S  E  P  A  T  R  H  R  D  W  E  K  R  L  G  A  R  A  Q  N  R  G  A
12302 CCTCGCACCGCCCCTGCCAGTACGCCCGCCGCAGCAGGTACCGGGGGGTCAGCCGGCCCGGGTCGATGTCATGGGTGACC
         >  L  A  P  P  L  P  V  R  P  P  Q  Q  V  P  G  G  Q  P  A  R  V  D  V  M  G  D
         <  E  C  R  G  Q  W  Y  A  R  R  L  L  Y  R  P  T  L  R  G  P  D  I  D  H  T  V
12382 GCGTGGTCCGGGAGCAGTTGCTCGCGGGCGCCGGCGGCCTTCATGGCGCTGATGAAGGAGGTGTCCTCC
         >R  V  V  R  E  Q  L  L  A  G  A  G  G  L  H  A  G  A  D  E  G  G  V  L
         <A  H  D  P  L  L  Q  E  R  A  G  A  A  K  M  A  S  I  F  S  T  D  E
12451 CCTGACTGGAGGTTGCCCCCGGTACGGCTGAGGGCCAGGTCGAAATCCAACCCGTGGGCGTGCGCGAAC
         >P  •
         <G  S  Q  L  N  G  G  T  R  S  L  A  L  D  F  D  L  G  H  A  H  A  F
12520 GCGGAGTCCACCCCCATGCACGCGCCCCAGATCTTGATGTTTCCCTGGTCACGGTGCCAGCCGACCAGGTGGAACTGGCCGGA
         <A  S  D  V  G  M  C  A  G  W  I  K  I  N  G  Q  D  R  H  W  G  V  L  H  F  Q  G  S
                                     junction marker
12603 GGTGACGTACCACGGCAGACGCAGCGCGGGGCGGGCCAGCCGGGTGCCGACCACGTGCGCGCCGTCGCGCAGGCTCTTGCGGACGGCGTCGA
         < T  V  Y  W  P  L  R  L  A  P  R  A  L  R  T  G  V  V  H  A  G  D  R  L  S  K  R  V  A  D  V
12695 CGGCAGCGGCGTCGAGCCGCACGTCGTCGTCGACGAACATCAGATGGTGGTGCGGCCAGCGGGCGAGCATCGCGTTGCGGGAGGCCGACAGG
         < A  A  A  D  L  R  V  D  D  D  V  F  M  L  H  H  H  P  W  R  A  L  M  A  N  R  S  A  S  L
12787 CCATTGGTGGCACCGAGGATGCGCATGGTGCCGCCGGCGGCCCGGACCTCCTCGGCGACCTCCTCCGCCTCGGCCGTGACGGGCCGGTCCAG
         <G  N  T  A  G  L  I  R  M  T  G  G  A  A  R  V  E  E  A  V  E  E  A  E  A  T  V  P  R  D  L
12879 CAGGACGTAGTACTCGTCGCCGGAGAGCTGGGCCATGTTGTGCGCGAGGTGTTTCCTGACGTTCTCCACCCGGAACGCGCAGATCGCCACCA
         < L  V  Y  Y  E  D  G  S  L  Q  A  M  N  H  A  L  H  K  R  V  N  E  V  R  F  A  C  I  A  V  V
12971 CCATCGGGTGGTCGGACGGATCGCGGCTGACCACAGAGGCGTTGTTCGGCATCGTCCCTCGACATGAGCGTTGTGGGGCCGGCGGGGAGA
         < M  P  H  D  S  P  D  R  S  V  S  A  N  N  P  M
13061 GGCGGCCCACCGGATCGCGCTCCGCGGCAGCGTGCCGCGGCCCCGGCCGCCCACGGACAGGTGGCGCACCGCAGCGCGGCGGGCCGTCCGG
13153 TGAGCGGCCGGGGGCGGAGCTCAGGCCGCTTCGTCCTTGCTGACGGTCGGCGGCCAGGTGCCCGCCGCGAGGATGCCCATCGCGTACGCCTT
13245 CGCGATCAGGGCCGGCCGGTTGGGCACTCGCAGGTTCTGCAACAGCTTGCTGACGTGGTACTCGACGCCCTGACGGCTGAGGTAGACCTTGT
13337 TGGCGATATGCACCGTCCGTTCGCCTGCGGCGATGCTTTCGATGATGCGCGCGTCCAGATCGGACAGTGAGAACTTGAGATTCACAACGCCC
13429 CCTTGATTGTGGATCGTGTTGGCTCGTACGCGGCCAGACGTCATCGCCCGGACACCCCCCTGAGGTGCCGGTGGACGAGTGGTTCGCTTCCGCT
13521 GGAAGACCGTCAGCGGCGGAAGGCCGGGTGCCCGCCACTCGTCGTCCTGCGCTTCGGCGGAGCTGTCTCAGTGTGCGGCGATGCCCCCGGCACG
13613 TAGCCCGCCTGACGGGCCTGTCGGCTTGGGCTCCAACTTCGGCAACCCATCGGTTCGCGCTGCACAGAACCAGCGGAGGAACATTGAGTTTC
13705 GAAGCCCTTCGCTACTGTCGATCGACATCACTGGCGAAATGAAACCGACCGGATTCGAGCCGATAGTTACGGAAAGTGACAATCGGCTGGCC
13797 CTGTCGCTCGCGCTGAACTCACCAATACGCCAAAAGCGTAGCCGGCCCACTGCGGAGCGTCCACCCCCCGAGGATATCGCCAGGCTTCCATG
13889 CAGAACTGGCAGGATCTTTCATCTCAGCCGCACCTGGCGACAAAACCCTGCTCAAGACCATGAGTAAGCAGGCGCGGGAAATCCATGCAGT
13981 GACATGTGTCACTTTAGACAACCCAGCTCCAGCCAGGCCCACCACCCTGACAAAAGGGCGGAATCGCGACCAGAGCGACACCAGCACATTC
14073 CTAGGGGATTCCTTAGTCTGGCGAGCGTCGATCCCCCACCCGTCAATCAATTGCCCGAACAAATTGCCCACCCGTCAAGATCAACCACTCCG
14165 CACCGTGAGCAGGCCGACCGTCCGGCAATGCGAACGACGACGTCCACCCCGTCCCGGTAGCCTCACCGCCGCTGGGGGGGGCACGGGCCCGGA
14257 CACCGTCCGGCGTCGTGATCAGCGGGTCGCTCGCCGGCTGTCGCCCCGCGCGGGGACCGGCATCGCGCGCGGGGCCGGCACGAAGATCTCCG
14349 GCGACCTGTCAGCCCTGCAAGCGGACCGGCATCGCGCGCGGGGCCGGAACCACCCGACGGTTCAGCGCCGGGACCGATCGGGAAGCCGACT
                                                          <  •  R  R  S  R  D  P  L  R  S
14440 CGCGGCCTCGTCCCAGAGACCCGCCCACCGCATCCCGCAGCGATCGTCGGGGCCGCCACCCGCAGCAGGTCAGCGCGGGCCCCGGGTCGACGC
         < A  A  E  D  W  L  G  G  V  A  D  R  L  S  R  R  P  R  W  G  L  L  D  R  A  P  G  P  D  V  R
14532 GGGCCCAGTCGACGACCTCCACCGAGCCGGGCCGATCCGGCAACTCCACCACCTCGGTCGGCACCCCGCTCACCTCGATCAACATCTCCACG
         < A  W  D  V  V  E  V  S  G  P  R  D  P  L  E  V  V  E  T  P  V  G  S  V  E  I  L  M  E  V
14624 AGGGAGCGGACCGGAACGGCCTCCCCCCGCCCCACGCCGATCACCCGCCGGTGACGGACTCCCGCGTGGCCGACACCACCGCCTCGGCGAC
         <L  S  R  V  P  V  A  E  G  R  G  V  G  I  V  R  G  T  V  S  E  R  T  A  S  V  V  A  E  A  V
14716 GTCCCGCACGTCGACGTAGTCCCGGTGGGCGCGCAACGGAGACAACTCCACCCTGGCCGACCGGTCGCGGCCCGCCGCGTCGACCAGGCGAA
         < D  R  V  D  V  Y  D  R  H  A  R  L  P  S  L  E  V  R  A  S  R  D  R  G  A  A  D  V  L  R  V
14808 CGACGACCCGCCCCAACAGGCTGTCGGGTGGCACGCCCGGACCCACCACGTTCGCGAGCCGCAGCACCGTCGCGTCCACCGAGCCGGCCCGC
         < V  V  R  G  L  L  S  D  P  P  V  G  P  V  V  N  A  L  R  L  V  T  A  D  V  S  G  A  R
14900 GTCGCCGCGAGCACGCCCTGGGTGGCGGCCAGCTTCGCCCTGCCGTACATGCTCTCCGGCTGGGTGGGCACCGTGGCACCGGCGGGGAGCCCC
         <T  A  A  L  V  A  Q  T  A  A  L  K  A  R  G  Y  M  S  E  P  Q  T  P  V  T  A  G  A  P  A  G
14992 GGGTGGCTCCTGGACGCGTTCCAGGACCGAGCCGAGGTGCACCAGCCTGGGCCGGCAACGGGTGCGCTCCAGCGCCGCGGTGACACTCCACG
         <P  P  E  Q  V  R  E  L  V  S  G  L  H  V  L  R  P  R  C  R  T  R  E  L  A  A  T  V  S  W  T
```

Figure 11D

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15084 TCGGGATCGTGCAGCTCGACGGCAGCTCGGCGTCCGTCAGGTTCCACTTGCCGCCGGTGGCGTTGACCACCGCGTCGGGCTGCTCGGCGTCG
        < P I T C S S P L E A D T L N W K G G T A N V V A D P Q E A D
15176 AACACGGCGGCCAGCGCGGCGGGGCTCCAGGGTGGCGACGTCCAGCGCCCGGGCCCGGTACGGCAGCCCCGCCGACGGGACGCGGCGGGCCAA
       <F V A A L A A P E L T A V D L A R A R Y P L G A S P V R R A L
15268 CACGAGGACGTCGTCGCCCCGGGCGGCAAGCGCGGCGCTCACGTGACGCCCGACGAAGCCCGTACCACCGGACGACCACGACACGCCGCGCGC
        < V L V D D G R A A L A A S V H R G V F G T G G V V V R R A G
15360 CCATCCGTACCTCCTGGGGATCAGTCTCGTGCGCCGGCGGCGTCCAGGCGACCGCCCGGCCCCTGACAGGTCACGGGGGCGCGCAACAC
       < M            < • D R A G A A D L R G G P G Q C T V P A R L V
15449 CCTGGCCCGGTCGCGAACCTCGTCCAGCAGCCGGGCCCGGGCGCGGATCGCCGTCACCTCCTCCGCCGGCTGACCGGCGGTGACGGCGCGGA
       < R A R D R V E D L L R A R A R I A T V E E A P Q G A T V A R V
15541 CGAACTCTCGCATCGTGTTGACGAACTGGTCCTCGGCCGGGAAGGTCAGCTCCCGCGTCTCGTCCTGCCGCTCCACCCGCACCACCGGGTGC
       < F E R M T N V F Q D E A P F T L E R T E D Q R E V R V V P H
15633 CAGGCCGGCCGGTGGGGTGTACGCCCGGTCGACGACGATCCGGCCGGCGCTTCCCCAGAGCTGGTACTCGCACCGGTAGGAGTGCTCGAAACC
       <W A P P P T Y A R D V V I R G A S G W L Q Y E C R Y S H E F G
15725 GAAGGCGATCTGTGCGGTCCGCCCGTCCGGCGTACACAACAGCGCGGCACCCGAAACGTCCACGCCGCGATCGGGGTCCTCCCGGAGGGTGG
       < F A I Q A T R G D P T C L L A A G S V D V G R D P D E R L T A
15817 CCGCCACCACCTCCGGCTCCTCCGGCAGGAAGAACCGGGCCGCGCCCAACGGGTAGACGCCCAGATCCAGCAGCGCTCCGCCACCCAGCTCG
       < A V V E P E E P L F F R A A G L P Y V G L D L L A G G G L E
15909 GGTCGGTAACGGATGTCGCCCGCAGGCAGCGGCGGAAACCCGAAGACGCCGGAGACCATCCGCAGCTCGCCGATCTCGCCGGCCGCGACCAT
       <P R Y R I D G A P L P P F G F V G S V M R L E G I E G A A V M
16001 CCGGCGCACGAAGTGGTGCACCCCATGTCGGAGGAAGGTGAGGTTGTCCATCAACACGAGCCCACGCGACCGGGCCTGGGTCAGCACCGCCG
       < R R V F H H V G H R L F T L N D M L V L G R S R A Q T L V A
16093 CGGTGTCGACCAGCCGGGTGGTCAGCGGCTTCTCCACCAGCACGTGTTGCCCGCGGCCAGGGCGCGTTCGATCCAGGTGTGGTGCAGCCCG
       < T D V L R T T L P K E V L V H K G A A L A R E I W T H H L G
16185 GTCGGCAGCGGAATGTAGACGGCATCGATGTCCGGGCGGTCGAGAACGGACTGGTAGCCCTCGGCGGCGGCGCACCCGAACTCCGCGGCGAA
       <T P L P I Y V A D I D P R D L V S Q Y G E A A A C G F E A A F
16277 GGCGCGGCCTTGGCCAGTTCCCGCGCCGGCCACCACGAGCTCCGCTCCGGGACCCGCCTGATCGCCGCAGGGCACGGCGGCCGCGGCCGC
       < A R A K A L E R A A V V L E A E P V R R I A P L A R R R A I
16369 TGTCGGCGCAGCCGAGAACCCCGATGCGGACCGTCATCTCCGCCATCGGGTCACCACAGGCTGCGCAGGCAGGCCAGCAAGCTGCGGGCC
       < D A C G L V G I R V T M E A M    < • W L S R L C A L L S R A
16459 TCGATGTTGAGGTAGTAGCCGTGCCGGAGCAGGGCCTCCAGCTGGCGCACCGTCACCCAGCAGAACTCGTCCGGCACCTCGGTCGGGAAGTC
       <E I N L Y Y G H R L L A E L Q R V T V W C F E D P V E T P F D
16551 GTCGCCGGCCGTCGACCAGGAGGTAACGGTTCTCGACCGGTAGAATCGCCCGCCCTCCTCGGTGAGCACGGTGTCGTAGAGGACGACCTCGG
       < D G A D V L L Y R N E S R Y F R G G E E T L V T D Y L V R E P
16643 GGGCGGCTTCCAGCACCTCGGCCAGGAACAGTGGTCGGGGGCCGGGCTGGTTGTCCGGGATGCACTGCACCGTTGGGCCCATCTCCATCGCG
       < A A E L V E A L F L P R P G P . Q N D P I C Q V T P G M E M A
16735 TCGAGCAGCCCCGCCTGGTAGCGCGCGTGCACCAGCAGGTGCGCCACTCCGTCGATTTCCTTGACCAGGAAGGCGACCACGCCCCGGTGCCG
       <D L L G A Q Y R A H V L H A V G D I E K V L F A V V G R H R
16827 CGGATACAACAGCGGCTGACTCCACCCGGTCACCTCGCGGTTGTCGATGCGCACCGTGACGCCGACCACGGAGAAGTGCCGGCCGGTCGTCCC
       < P Y L L P Q S W G T V E R N D I R V T V G V V S F H R G D D R
16919 GCGCGATCCCGTCCGCGGTGTGCCGCCAGTCCGGCAGCCCTCGTAGCGGCACCCGCCGCACGGTCATCTCGTGCCGGCCCTTGGCCCCGGTG
       < A I G D A T H R W D P L G R L P V R R V T M E H R G K A G T
17011 AACCAGCTCAACACCGACACCAGGTCGTGGCGGCCGGGGGCGCCCGCCGCCGAGCGCACGATCGCCGCCACCGCCGGCGACGACGGCGCCTC
       <F W S L V S V L D H R G P A G A A S R V I A A V A P S S P A E
17103 GGTCTCCTGGGCCGCGGCGTAGAAGGCGAGGGCAGACATGACAGCACCGTACGCGTGTCCATGTTGACCAGGCCGTCCACCCGCAGCAGCG
       < T E Q A A A Y F A S P L C S L V T R T D M N V L G D V R L L A
17195 CGAGCAGTTCGCGCAGCGGGAGCCACCGGTGGTAGTCGCCGGCCGGCACGTCCTCGTCGACCTGGACCACCATGTTCCGGTTGCGCTTGCGC
       < L L E R L P L W R H Y D G A P V D E D V Q V V M N R N R K R
17287 AGGAACCAGGAGCCCTGCTCCGACTGCAGGACGTCAACCAGCACCCGACCGGCCCCGGGCGGGTGAAGTAGTCGAGGTACTTCGTGCCGCC
       <L F W S G Q E S Q L V D V L R G A G P R T F Y D L Y K T G G
17379 GCCACGGTGCACCCGGGTGTAGTTGCTCCGGGTGGCCTGCACCGTCGGCGAGAGCTGCATGACGTTGATGTTGCCGGGCTCCACCTTGGCCT
       < G R H V R T Y N S R T A Q V T P S L Q M V N I N G P E V K A Q
17471 GGAGCAGGCAGTACGGTGTCCCGTCGACGACCTTGACGAGCATGCCGAGGATGCCGATCTCCGGCTGGTTGATGATCGGCTGGTGCCATTCG
       < L L C Y P T G D V V K V L M G L I G I E P . Q N I I P Q H W E
17563 CGCACCGCGCCGTAGGTGGTCTGGACGGTGCAGCCCTCGATCACGAAGAACCGGCCGCTCTCGTGCCCGAGGTTGCGGTCACCGGTCGAA
       <R V A G Y T T Q V H L G E I V F F R G S E H G L N G T V P D F
17655 CGCCCACCCGGGCAGCCGGTCCAGCGGCACGCGGTCCACCCGGCAGTAGGTCGACCGGGTCCGCTCGGCGAACCAGGAGAGGAAGTCCGGCC
       < A W G P L R D L P V R D V R C Y T S R T R E A F W S L F D P R
17747 GGACCCCTCGGCGTGCAACGCCGACCACGAGCCGCCGTCGACCGGGCCGGGCCGGTGCGGGCCCGCGTCCCGGGTCAGCAACGGCCCGTCG
       < V G E A H L A S W S G G D V P G R H P G A D R T L L P G D
17839 GCGCGGACCTTCGGGTCGGGCGACGAATCGCTCACCACAGCTCGGCCAGTTCGGCGGAAAAGGCGTGGGAAGACCCGTCCGTGTCCGCCAA
       <A R V K P D P S S D S V
                           < • W L E A L E A S F A H S S G D T D A L
17930 CAGGCGCAGATCGCTGTCGACCATCATGGCGACCATCTCCTCGAAGGAGACGGAGGGTTTCCAGCCGAGCCGCTGGCGGGCCTTCGTCGGAT
       < L R L D S D V M M A V M E E F S V S P K W G L R Q R A K T P D
18022 CCGCGCAGAGCAGCTCGACCTCGGCGGGCCGGATGAGCGGACTCGTCCACCACCACGTGGTCCCGCCAGTTGAGGCCCACGTGGGCGAAGGCC
       < A C L L E V E A P R I L S E D V V V H D R W N L G V H A F A
18114 GCCTCGACCAGCTCGCGGACGCTGTGCGTGACCCCCGTGCCGAGGACGTAGTCCTCCGGCTCGTCCTGGGCCAGCATCAGGACCATGCCCCG
       <A E V L E R V S H T V G T G L V Y D E P E D Q A L M L V M G R
18206 CACGTAGTCGCCCGCGAAGCCCCAGTCCCGCTCGGCCGAGAGGTTGCCCAGGCGAAGCGAGCTGCGAATGCCCAGCTTCACCGCCGCCACGC
       < V Y D G A F G W D R E A S L N G L R L S S R I G L K V A A V G
18298 CCAGCGACACCTTGCGGGTGACGAACTCGGGACCACGCACCGGTGATTCGTGGTTGAACAGAATGCCGGAGACGGCATACATGCCGTACGAC
       < L S V K R T V F E P G R V P S E H N F L I G S V A Y M G Y S
18390 TCACGGTAGTTCTGCACCATGTAATGCCCGAACGCCTTGGCCGCGCCGTACGGGCTACGCGGATGGAACGGGGTCAGCTCATTCTGGACGGG
       <E R Y N Q V M Y H G F A K A A G Y P S R P H F P T L E N Q V P
18482 CTCCCCGCACCTTGCCGAACATCTCCGACGAAGACGTCTGATAAAAGCGCGGCTGACCGGCTGCGGGACTGCGGGAATCCGACAGGCCCCGA
       < E R V K G F M E S S S A Q Y F R P Q G A A P S R S D S L G G V
18574 CGATCCGCAAGGCTTCGAGCATGCGGAGCACACCCATGCCGGTGACCTCCGCCGTCGTGGTGGACTGCCGCCACGACACCGGCACGTACGAC
       < I R L A E L M R L V G M G G T V E A T T T S Q R W S V P V Y S
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Figure 11E

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18665 AGCGCGCCGAGGTTGTAGACCTCGTCCGGCGCCGCGCGTTCGATCGCCGCCACCAGGCTCGTCTGATCCAGAAGGTCGCCGCTGATCAGCTT
      <L A G L N Y V E D P A A R E I A A V L S T Q D L L D G S I L K
18758 GACCGCTGGATCAGGTTGCCGAAGGCTGCGGACCGAGGGCGCGGTCTGCCCGCGCACCAATCCAAATACCTCGTATCCGGACTGAAGCAGGT
      < V A P D P Q R L S R V S P A T Q G R V L G F V E Y G S Q L L H
18850 GCTCCGCGAGATACGTGCCGTCCTGGCCGGTAATTCCAGTGATCAGCGCCCGCCGTGTCAGGGTAGTCTCCAGCCGTGAAGCCACCTGGCC
      < E A L Y T G D Q G T I G T I L A R R T L T T E L R S A V
18941 GAGGCGTGACCTCGCGCCGATGGCGGACCAAAGATCCGCCCGTTCGAAATGGGGTCGGATCTCCCGCTACCGCGCTCACGGTACGCGAATCT
19033 CCAAGCGGATTCAGCGACCCGGAAAGCAATATAGGGAGGTTACTAGTAGTACTTTCCGGCGGGCCGGCAGCGACGCCCGGCCCGGACCGGCA
19125 GGATCGCCCGTTCGGCCGGCGGACCCATCCCGGACACCTTCCACCGAAGCTCTTCGGGATCGTCGCCCGCCGATGCGAACTGCTTGACTCC
19217 ACCGTTTTGTCCCCCTAACGTCGGCGAGGCTGCCAGCCGGCCCGCGAGCCGGGCCGGGTTCACGAAGGCGCCAACTTCCGGTGAGAGAGCAG
19309 GGCTCATGTCGCAGAGCCGGCCCGCGGCCGCAGCACCCCAGCCCGCCTGCCACGTCGCCGCGCCATGGTCGCGTTGGTCGCGGTGATGAT
                                                                      >M V A L V A V M I
19400 CCCGATGGTGCTGGCCACCCTCGACAACACCATCATCGGCACCGCACTGCCCACCGTGGTCGGCGAGTTGGGCGGCCTCAGCACGCTCTCCT
      > P M V L A T L D N T I I G T A L P T V V G E L G G L S T L S
19492 GGGTGATCACCTCGTACACGCTGGCCACGGCCGCCTCCACGCCGGTCTGGGGCAAGCTCGCCGACATGTACGGCGGCAAGGTGGTCTTCGTG
      >W V I T S Y T L A T A A S T P V W G K L A D M Y G G K V V F V
19584 GCCACGCTGGTCGTGTTCCTGGCCGGGTCGCTGCTGTCCGGCATGGCGCAGAGCATCACCCAGCTGACCGTCTTCCGGGCCGTGCACGGGCT
      > A T L V V F L A G S L L S G M A Q S I T Q L T V F R A V H G L
19676 CGGCGCGGGCGGCCTGATGGTCTGCGCGTTCGCCATCATGGTGGAGGTTCTCGCCGGCCCTGACCTGCCCAAGTACCAGGGCATCATGTCGG
      > G A G G L M V C A F A I M V E V L A G P D L P K Y Q G I M S
19768 CGACCATGGGCCTGACCATGGTGGCGGGCCCGCTCGTCGGCGGCCTGATCACCGATGAGCTCGGCTGGCGCTGGTGCTTCTACATCAACCTG
      >A T M G L T M V A G P L V G L I T D E L G W R W C F Y I N L
19860 CCGATCGGGGCGGTCGCGCTGCTCATCGTGGTGCTGATGATGCACCTGCCGCGCCGACACACCAAGGCCCGGATCGATTACGCGGGTGCTGC
      > P I G A V A L L I V V L M M H L P R R H T K A R I D Y A G A A
19952 CCTGCTCACCGTGGTCAGTTCGTGCGTCGTGCTGGTGACCACCTGGGGCGGCATCACCTACCCCTGGGCGTCTCCGATGATCCTGGGGCTGG
      > L L T V V S S C V V L V T T W G G I T Y P W A S P M I L G L
20044 TCGCGCTCGGGGTGCTGACCTGCGCGCTCTTCGTGGTGGTCGAGCGACGGGTGGCCGAGCCGTTGGTGCCCCTGGCCATGTTCCGGCAGCCTG
      >V A L G V L T C A L F V V V E R R V A E P L V P L A M F R S L
20136 AACTTCACCCTGAGCACCCTCATCGCCTTCCTGGTCGGCTTCGCCCTCATCGCGGGGCTGACCTTCCTGGCCCTGTTCCAGCAGGCGGTGCA
      > N F T L S T L I A F L V G F A L I A G L T F L A L F Q Q A V Q
20228 GGGTGCCTCCGCGTCCGACTCCGGCCTGTTGCTGCTGCCCCTGCTGCTGTCCATGGCGGCGGTCAACGTGGTCGGGGGTCGCCTGATGAGCG
      > G A S A S D S G L L L L P L L L S M A A V N V V G G R L M S
20320 GCGGGCGTTCCTACCGGCTGCTGATGCTCGCCGGTGCGGCGCTGATGACCCTGAGCCTGCTGCTCTTCGCCCTGATGGACGTGGGCACCAGC
      >G G R S Y R L L M L A G A A L M T L S L L L F A L M D V G T S
20412 CGGACGGTCACCGCGATCCCCATGGTCGGCTTCGGCGCAGGGCTGGGGCTGCTCATGCAGACCAGCCTGATGGTGGCGCTGAGCAGCGTGGA
      > R T V T A I P M V G F G A G L G L L M Q T S L M V A L S S V E
20504 GATGAGGAACCTCGGGGTGGCCGCGTCCACGTCCACGCTCTTCCGCACCATCGGTGGGGCGGTGGGGGCGTCGGCGACGGTCTCGCTGTTCT
      > M R N L G V A A S T S T L F R T I G G A V G A S A T V S L F
20596 CCGTGCGGGTGCAGTCGGCGCTGGCCGATCGGGGGGTCGCCGACGTGGCTGACCTCCTCGGCCACTCCGCGGCTGGACGGCGCCGGGGCTG
      >S V R V Q S A L A D R G V A D V A D L L G H S A R L D A A G L
20688 GCCCAACTCCCCCGGGCCGTCCGTGTCCACTTCATGCACGCGGTGGCCTCCGGCACCCGGTGGGCCTTCCTGATGACCGTGCTGGCGGGGCT
      > A Q L P R A V R V H F M H A V A S G T R W A F L M T V L A G L
20780 GATCTGCGTCGCCGGCGGCGTGGTTCCTGCGCCGGGTCACCCGTTGACGTCGGCACCGGTGGCACCCGAACCGGCGCGACGTCGCCGCGC
      > I C V A A W F L R R V T P L T S A P V A P E P A R D V A A
20872 CCGCCGCCAGCAGCGGGCGCGCGCCGAACTACTAGCGGATTTCCTAGGGTTCCTCGTCGACGGTAGAGCTGAATTCACCGGCGACCTAACA
      >P A A S S G R A P N Y •
20963 TTCTTTTCGCGATCCGGAATCCGTCCATTCCCCTGTCTGGCGATGGTCGACGGGCCGGCCCGTGCCGAGCGGACAGACACAGATTCTCGGAT
21055 TGGAGCTCGATGTCCAGCAAGATCCTAGTCATCGGTGGAGGTCGGCCGGATCCACGGCCGCCGCGCTGCTCGCCCGATCGGGGCTGTCG
              >M S S K I L V I G G P A G S T A A A L L A R S G L S
21145 GTGACGCTCCTGGAAAAGGAGACGTTCCCGCGATACCACATCGGCGAGTCGATCGCGTCCTCGTGCCGCACCATCGTCGATTTCGTGGGCGC
      > V T L L E K E T F P R Y H I G E S I A S S C R T I V D F V G A
21237 TCTCGACGAGGTCGACTCGCGGGGCTACCCGCAGAAGAACGGGGTCCTGCTGCGCTGGGGCAACGAGGACTGGGCCATCGACTGGGCCAAGA
      > L D E V D S R G Y P Q K N G V L L R W G N E D W A I D W A K
21329 TCTTCGGTCCGGGCGTGCGGTCCTGGCAGGTCGACCGGGACGACTTCGACCACGTCCTGCTGCTCAACAACGCCAAGCAGGGCGCCAAGATC
      >I F G P G V R S W Q V D R D D F D H V L L N N A G K Q G A K I
21421 ATCCAGGGCGCGGCTGTCAAGCGGGTGTTGTTCGACGGTGAGCGGGCCACCGCCGCCGAGTGGTTCGACCCCGAGTCGGGTGAGGTCCGCAC
      > I Q G A A V K R V L F D G E R A T A A E W F D P E S G E V R T
21513 CATCGATTTCGACTACGTGGTCGACGCGTCCGGCCGGGCCGGGCTGATCCCGTCCCAGCACTTCAAGCACCGGCGCCCCACCGAGACGTTCA
      > I D F D Y V V D A S G R A G L I P S Q H F K H R R P T E T F
21605 AGAACGTGGCCATCTGGGGCTACTGGCAGGGTGGCTCGCTGCTGCCGAACTCTCCCTCCGGCGGGATCAACGTCATCTCCGCGCCCGACGGC
      >K N V A I W G Y W Q G G S L L P N S P S G G I N V I S A P D G
21697 TGGTACTGGGTCATTCCGCTGCGCGGCGACCGGTACAGCATCGGCTTCGTCTGCCACCAGAGCCGCTTCCTGGAGCGGCGCAAGGAGCACGC
      > W Y W V I P L R G D R Y S I G F V C H Q S R F L E R R K E H A
21789 CTCGCTGGAGGACATGCTCGCCGCACTGGTGTACAGGAGTCCCCGACCGTGCGGCCTGACGGCGAACGGGACGTACCAGCCGGGCGTGCGGG
      > S L E D M L A A L V Q E S P T V R G L T A N G T Y Q P G V R
21881 TGGAGCAGGACTTCTCGTACATCTCCGACAGCTTCTGCGGGCCCGGCTACTTCGCGGCCGGCGACTCCGCCTGCTTCCTGGACCCACTGCTG
      >V E Q D F S Y I S D S F C G P G Y F A A G D S A C F L D P L L
21973 TCCACCGGCGTGCACCTCGCCCTCTACAGCGGCATGCTCGCCTCGGCGTCCATCCTGGCCACCATCCACGGTGACGTCACCGAGGAGGAGGC
      > S T G V H L A L Y S G M L A S A S I L A T I H G D V T E E E A
22065 GCGGGCGTTCTACGAGTCCCTCTACCGCAACGCCTACCAGCGCCTGTTCACCCTCGTCGCCGGCGTCTACCAGCAGCAGGCCGGCAAGAGGG
      > R A F Y E S L Y R N A Y Q R L F T L V A G V Y Q Q Q A G K R
22157 CATACTTCGGCCTGGCCGACGCGCTGGTGCACGACAGCGGCGAACCCGAGTACGAGAAGGTAGACGGGGCCCGCGCCTTCGCCCAGCTCGTC
      >A Y F G L A D A L V H D S G E P E Y E K V D G A R A F A Q L V
22249 GCCGGCCTCGCCGACCTGGACGACGCGGCGGAGGGACGGCACGACAGCACCGCGGCGGCGGCACCGGCGGAGCAGGACAACTCCGTCCGGCA
      > A G L A D L D D A A E G R H D S T A A A A P A E Q D N S V R Q
22341 GCTCTTCCTGGCCGCGGAGGAGGCCCGGCGGATGGCCGACGCGCGCACGCCGAGCGCCCCGGTCAGCGAGGCGCCGGGCAAGCTCGACAGCC
      > L F L A A E E A R R M A D A R T P S A P V S E A P G K L D S
22433 ACGACCTCTTCGACTCGGCAACCGGCCTCTACCTGGTCACCACCCCGCGACTGGGGATCCGCCGGGGCCAAGCCGGCCGACACGCAGGCGGCG
      >H D L F D S A T G L Y L V T T P R L G I R R A K P A D T Q A A
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Figure 11F

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22525 GCAGAGCAGTCTGCCTGAGGTTCCACCCCTGGTGGCCCCCGGCCCGGACCGCGCCGGTCCGGGGGCTGCTCAACCCTCCCACCAACATCCG
       > A  E  Q  S  A  •
22616 GCATCCGGTGCCGGCGGCTGAGCAGGGGCAGCGCCACCGACTCCGGCCCGTCACATGGACAAGGTCACCTCTCCCGTGCTGAACAGACGACA
22708 GTTGCTCGCCCTCGGCAGCGTGGCCGCCGGAGGCACCGTCATGTCACGCTCCCTCAGACGGGACGCGCAGGCCGCCCAGGCGGCACCGGC
                                          > M  S  R  S  L  R  R  R  D  A  Q  A  A  Q  A  A  P  A
22798 GTCGCCCGCCAACCCGCACGCCGGGCACGCCGCCCGGTGCCCAGCCGGGTCAGCACGACCACGGTCGCGGTCACCCCGTTCACCGAGCCGA
       > S  P  A  N  P  H  A  G  H  A  A  P  V  P  S  R  V  S  T  T  T  A  V  T  P  F  T  E  P
22890 TGCCCGTCCCGCCGCGGCTGACCCCGGTCTCCCGCCGCGACGGCATCGACGTCTACGAGATCCCCATCCGGCCGGCGCAGGTGCAGATCCTG
       >M  P  V  P  P  R  L  T  P  V  S  R  R  D  G  I  D  V  Y  E  I  P  I  R  P  A  Q  V  Q  I  L
22982 CCCGGCCTGCTCACGCCCGCCTACACCTACGCCGGTTCCTTCGTCGGCCCCACCATCCGGCCGGCCACGGGCCGGCCCGTGCGGATCACCTA
       > P  G  L  L  T  P  A  Y  T  Y  A  G  S  F  V  G  P  T  I  R  A  R  T  G  R  P  V  R  I  T  Y
23074 CACCAACGGGCTCGACACCCACGCCAACGTGCACCTGCACGGCGGGCACGTGCCGGCCACCAGCGACGGTCACCCGATGGACCTGATCCCGC
       > T  N  G  L  D  T  H  A  N  V  H  L  H  G  G  H  V  P  A  T  S  D  G  H  P  M  D  L  I  P
23166 CGGGCGGCTCGAAGGTCTACGACTACCCGAACCTTCAGCGCGGCGCGACGCTCTGGTACCACGACCACACCCACGCCTACGAGGCCGACCAC
       >P  G  G  S  K  V  Y  D  Y  P  N  L  Q  R  G  A  T  L  W  Y  H  D  H  T  H  A  Y  E  A  D  H
23258 GTCTACCGCGGACTGCACGGCTTCTATCTGATCGACGACCCGGCCGGCATCACCTGCGCCTGCCCGCCGGCAAGTACGACGTGCCGATCAT
       > V  Y  R  G  L  H  G  F  Y  L  I  D  D  P  A  E  H  H  L  R  L  P  A  G  K  Y  D  V  P  I  M
23350 GCTGCGCAACGCCCAGTTCGACGACTCCGGCGCCCTCGTCTTCGGCCACCCGGACGACGGGTCACCATCCTGGCGAACGGCAAGGCCCAGC
       > L  R  N  A  Q  F  D  D  S  G  A  L  V  F  G  H  P  D  D  R  V  T  I  L  A  N  G  K  A  Q
23442 CCTACTTCGAGGTGGCCCCGCGCAGGTACCGGTTCCGCCTGCTCAACGCGGCGCTGAAGCACGTCTTCCGGCTCAACCTGGGCGGCGAACCG
       >P  Y  F  E  V  A  P  R  R  Y  R  F  R  L  L  N  A  A  L  K  H  V  F  R  L  N  L  G  G  E  P
23534 CTCACCCGCATCGCCACGGACGGCGGGCTGCTGCCCGCCCCCACCAGTCACACCGAGCTGGCGCTCTCCTCCGGGGAGCGGGTCGAGATTGT
       >L  T  R  I  A  T  D  G  G  L  L  P  A  P  T  S  H  T  E  L  A  L  S  S  G  E  R  V  E  I  V
23626 GATCGACTTCGCCGAGCACGCAGGCGGCGGGGCCGGTCTACCTCTACGACGGGGACAACCCGATCCTGCGCTTCGACGTGTCGTCCCGGGCGG
       > I  D  F  A  E  H  A  G  G  G  P  V  Y  L  Y  D  G  D  N  P  I  L  R  F  D  V  S  S  R  A
23718 TCACCGACCCCAGCCGGGTGCCGGTCACCCTGCGCGCACTGCCCCCGATGGGCACGCCGACCGTGGAGCGCACCGTGTCGATGAGCTTCGAC
       >V  T  D  P  S  R  V  P  V  T  L  R  A  L  P  P  M  G  T  P  T  V  E  R  T  V  S  M  S  F  D
23810 ATGTCGGCCCGGCCCCGCGATCGCGCTCATGGACGGCAAACCGTTCGACCCTCTCCGGGTGGACGTACAGGTCAAGCGGGGCAGCACCGAGAT
       > M  S  A  R  P  P  I  A  L  M  D  G  K  P  F  D  P  L  R  V  D  V  Q  V  K  R  G  S  T  E  I
23902 CTGGAACGTGGTCAACGCGGATACCGATCCGTTCCCCTTCGACCATCCGTTCCACCTGCACCTGGTGACGTTCCGGGTGCTCGGCCGCGACG
       > W  N  V  V  N  A  D  T  D  P  F  P  F  D  H  P  F  H  L  H  L  V  T  F  R  V  L  G  R  D
23994 GCGGGCCGCCCGGCCCGGAGGACGCGGGCTCAAGGACACCGTCTACGTCTCGCCCAAGGGGTCTGTCAAGATCCAGGTCACCTTCGCCACG
       >G  G  P  P  A  P  E  D  A  G  L  K  D  T  V  Y  V  S  P  K  G  S  V  K  I  Q  V  T  F  A  T
24086 CCGTACCTCGGGCAGTACGTCTACCACTGCCACTACCTGGAGCACTCGTCGCTGGGGATGATGGCCCAGCTGGAGGTTGTGCCCTGAGGGC
       > P  Y  L  G  Q  Y  V  Y  H  C  H  Y  L  E  H  S  S  L  G  M  M  A  Q  L  E  V  V  P  •
24177 TCAGCCGTGCAGGTCGACGATCGAGGGGTGGGCGCCGAACAGGCTGACCGGCCGCACGTCGCCCACCCCGAACCCGGCGGCGCGGGCCAGG
       < •  G  H  L  D  V  I  S  P  H  A  G  F  L  S  V  P  R  V  D  G  V  G  F  G  A  A  R  A  L
24268 TCGGCCTGGTCGGCGAACTCGTGCAGCAGCAGTACCGCCGCCGGCCGTCACCCGGCCAGCTCCGGCGGAAGAGGCGGCCGGAATC
       <D  A  Q  D  A  F  E  H  L  L  L  V  A  R  G  G  D  V  T  V  R  R  L  E  A  F  L  R  G  S  D
24360 ACCGGCGAGCACGCCCCGCGCCTGCACCTGCCGGTCCCAGGGCGGATTGCTGACCACCCGGTCCACCCGACCGGTCCGCAGCGGCAATCGTC
       < G  A  L  V  G  R  A  Q  V  Q  R  D  W  P  P  N  S  V  V  R  D  V  R  G  T  R  L  P  L  R  G
24452 CGGCGTCGGCGACCGCCCAGGTGACGCGGGCCCCCGACGCCGCCGAGTTGGCGACGGCCGCGCCGACCGTCTCCGGGTCGTGGTCCGAGCCG
       < A  D  A  V  A  W  T  V  R  A  G  S  A  A  S  N  A  V  A  A  G  V  T  E  P  D  H  D  S  G
24544 AACAGCACCGCCCCCGGTGCCAGCCCGGCTGCCTCCACGGGGATCGTGCCGGTGCCGCAGCACGGATCGGCCACCAGCATCCCGGGGCGGAT
       <F  L  V  A  G  P  A  L  G  A  A  E  V  P  I  T  G  G  T  G  C  C  P  D  A  V  L  M  G  R  I
24636 GCCGGCCAGCCAGGCCAGCGCCGCGGCGAGCGGCGGATGCAGGGTCCCCGGCGTGGACGACCGCTTGTAGGCCCGCCGGTGCAGCGGCCGGT
       < G  A  L  W  A  L  A  A  A  L  P  P  H  L  T  G  P  T  S  S  R  K  Y  A  R  R  H  L  P  R  D
24728 CGGCCACCCGTACCGCCAGCGTCGCCTGGGTGCCCTCGACGGTGACCGCAGCGACAGCCCGCCCTCCGGCGGGGCCTCGCCGCCGCGGCGG
       < A  V  R  V  A  L  T  A  Q  T  G  E  V  T  V  R  L  S  L  G  G  E  P  P  A  E  G  G  R  R
24820 GAGTGGTAGCGCAACCCGAGCGCGGCCACCGCGTGCCGCCCCACGCGTCCTCGATGTCGTACCGGTTGTAGTTGCGGCGGCCGAGGAAGGA
       <S  H  Y  R  L  G  L  A  A  V  A  H  R  G  V  A  D  E  I  D  Y  R  N  Y  N  R  R  G  L  F  S
24912 GGCGGCGACGTCCACGGTCGCCGGCCGCCCGGGCACGCCGCAGGCGGCGCGGGCCGGCAGCACCGCCGGCAGCGCCGCCGCCCGGGCCAGCC
       < A  A  V  D  V  T  A  P  R  G  P  V  G  C  A  A  R  A  P  L  V  A  P  L  A  A  A  R  A  L  R
25004 GGGTGAAGGCCGCCAGGTCCGCCTTGGTGTGGCCGACGCCGTCGGCGACGGCGACGAGCAGGACAGGTCGTCGACGGTACGCAGATCCAGC
       < T  F  A  A  L  D  A  K  T  H  G  V  G  D  A  V  A  V  L  L  F  L  D  D  V  T  R  L  D  L
25096 AGGCGCGGCTCCGCGCTGGCGGCGGAGAACCACACCTCGCGGTGCCGGCGGTGCTCGACCCGGCCGAGGCCCCGCTCCTCGATCTCCTGGGC
       <L  R  P  E  A  S  A  A  S  F  W  V  E  R  H  R  R  H  E  V  R  G  L  G  R  E  E  I  E  Q  A
25188 GGCCACCTCCTCCAGCCCTCGCAGGGTCCGTGCCATGAAGCGCACCGTCACCGTCCGCCGATCCTCTCCCCGCCGGGTCGTCCCGCCGCC
       < A  V  E  E  L  G  R  L  T  R  A  M
25278 GTGCCGGCGGCGTCCGCGAGCTACCCACCGCCACCGCCGCCGGGACGCAGCCGACGCCGACCGGACCCGCCGACGGGGGAGCCGACGCCGA
25370 CCGGACCCGCCAAGACTAGGTGAACCTCTATAGGAATTCGCGTGCCCCCTTCATAGGGTCCGAAAGGGGTAATGGAACCGTCCGGCACCGGA
25462 CGGCTCGTTTTCTTCCCCCAATTCCGTCCGTCCGACCTGAGCCGTCGCAGGGAAGGCGAGGCCGAGCAGTCGAGCAGTTGATCGGTCGATG
                                                                                                 > M
25553 CCGCACGGGCCCGTGCGCCGAAATCGTGGAGATTGCGCAGTGCGTACACCGGATCTGTTCATCGGCGCCGTCGGCGCCTTCGTCCCGCCGAC
       > P  H  G  P  V  R  R  N  R  G  D  C  A  V  R  T  P  D  L  F  I  G  A  V  G  A  F  V  P  P  T
25645 GGTGAGCGTCGAGTGGGCGATCGACCGCGGTCTTTACTCCCGCGAGCAGGTGGAGCTGCACGAGCTGGCGGGCACGGCCATCGCCGGCGACC
       > V  S  V  E  W  A  I  D  R  G  L  Y  S  R  E  Q  V  E  L  H  E  L  A  G  T  A  I  A  G  D
25737 TGCCCGCGCCGGAGATGGCGCTGCGCGCCGCCCAACAGGCGGTCAAGCGCTGGGGCGGCTCGCCGACGGAGTTCGACCTGCTGCTCTACGCC
       >L  P  A  P  E  M  A  L  R  A  A  Q  Q  A  V  K  R  W  G  G  S  P  T  E  F  D  L  L  L  Y  A
25829 AGCACCTGGCACCAGGGGCCCGACGGCTGGCCGCCGCACTCCTATCTCCAGCGGCACCTGGTCGGCGGCGACCTGCTGGCGTTGGAGATCCG
       > S  T  W  H  Q  G  P  D  G  W  P  P  H  S  Y  L  Q  R  H  L  V  G  G  D  L  L  A  L  E  I  R
25921 GCAGGGCTGCAACGGGATGTTCAGCGCGTTCGAGCTGGCCGCCAGCCACCTCCAGGCGGTACCGAGCGCACCAGCGCCCTGCTGGTCGCCG
       > Q  G  C  N  G  M  F  S  A  F  E  L  A  A  S  H  L  Q  A  V  P  E  R  T  S  A  L  L  V  A
26013 CCGACAACTACGGCACCCCGATGGTCGACCGCTGGCGGATGGGCCCCGGCTTCATCGGTGGCGATGCCGGCAGCGCCCTCATCCTCACCAAG
       >A  D  N  Y  G  T  P  M  V  D  R  W  R  M  G  P  G  F  I  G  G  D  A  G  S  A  L  I  L  T  K
26105 CGACCCGGCTTCGCGCGGCTCCGCTCGGTCTGCACCAAGTCGGTCCCGGAGGCCGAGCGGCTGCACCGGGGCGACGAGCCGCTGTTCCCCCC
       > R  P  G  F  A  R  L  R  S  V  C  T  K  S  V  P  E  A  E  R  L  H  R  G  D  E  P  L  F  P  P
26197 GAGCGTCCTGACCGGCCGGGAGCTGAACTTCACCGCCCGGATCGACCAACAGTTCGCCGCCCGCAGCCCCGCCTCGATCGCCATGGCGGACG
       > S  V  L  T  G  R  E  L  N  F  T  A  R  I  D  Q  Q  F  A  A  R  S  P  A  S  I  A  M  A  D
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Figure 11G

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26289 TCGGCGACCACATCGAGGAGGTCGTGGGGCGCGCCCTCGCCGAGGCGGAGATCGAGGTCGGCGACCTCGCCAGGGTCGCCTTCATGAACTTT
      >V  G  D  H  I  E  E  V  V  G  R  A  L  A  E  A  E  I  E  V  G  D  L  A  R  V  A  F  M  N  F
26381 TCCCGGGAGATCATGGAGCAGCGCTGCCTGGCCAACTGGGGCCTGCCCATGAGCCGGTCCACCTTCGACTTCGGTCGCCGGATCGGGCACTG
      >  S  R  E  I  M  E  Q  R  C  L  A  N  W  G  L  P  M  S  R  S  T  F  D  F  G  R  R  I  G  H  C
26473 CGGGGCGAGCGACCCCTTGCTGGCCCTGGAACACCTGGCCAGGACGGGGGGCCTCGGCCCCGGCGATCACCTGCTGACCCTCGGCACCGCGC
      >  G  A  S  D  P  L  L  A  L  E  H  L  A  R  T  G  G  L  G  P  G  D  H  L  L  T  L  G  T  A
26565 CGGGCGTGGTGGTGTCGTGCGCGATCGTCCAGGTGATCGAGTCGCCGACGTGGCGGGAGTGACCCGCTGGACACCTGCGGCGGCCCGCCCA
      >P  G  V  V  V  S  C  A  I  V  Q  V  I  E  S  P  T  W  R  E  ∘
26656 GCCCAGCAAACCGACAGCAGGGGATGATTGTGGAAGCAGAGAAGGACCGGTTGCGTCCGGTGGCGTCCGAGGCGGTCGCCGTGGTGGGGA
                          >  V  E  A  E  K  D  R  L  R  P  V  A  S  E  A  V  A  V  V  G
26746 TCGGCTGCCGGTTCCCGGGCGACGTCAACTCGCCCGACGAGTTCTGGGACCTGCTCACCGGGGGTCGCAACACCACCGGGACGGTGCCCGAG
      >I  G  C  R  F  P  G  D  V  N  S  P  D  E  F  W  D  L  L  T  G  G  R  N  T  T  G  T  V  P  E
26838 GAGCGCTGGAGCGCGTACCGCGACCTGGGTCCGGCGTTCGAGTCCGCGCTCCGGTCGGCCACCCGGGCGGGCAACTTCCTGGCCGACATCTC
      >  E  R  W  S  A  Y  R  D  L  G  P  A  F  E  S  A  L  R  S  A  T  R  A  G  N  F  L  A  D  I  S
26930 CGGCTTCGACGCGGACTTCTTCGGCATCTCCCCGCGCGAGGCCGAGCTGATGGACCCGCAGCAGCGGCTCATGCTGGAGGTGACCTGGCAGG
      >  G  F  D  A  D  F  F  G  I  S  P  R  E  A  E  L  M  D  P  Q  Q  R  L  M  L  E  V  T  W  Q
27022 CGCTGGAGGACGCCGGGATCCCGCCCCGCACCCTGGCCGGCACCGACGTCGGCGTCTTCGCCGGCGTGTGCACCTACGACTACGGCGGCCAC
      >A  L  E  D  A  G  I  P  P  R  T  L  A  G  T  D  V  G  V  F  A  G  V  C  T  Y  D  Y  G  G  H
27114 CAGTTGGAGGACCTGCCGCACATCGACGCCTGGACGGGCATCGGCGCCGCCACCTGCGCCGTCGCCAACCGGGTCTCCCACGTGCTCGACCT
      >Q  L  E  D  L  P  H  I  D  A  W  T  G  I  G  A  A  T  C  A  V  A  N  R  V  S  H  V  L  D  L
27206 GCGCGGGCCGAGCCTGTCGATCGACACCGCCTGCTCGGCGTCGCTGGTCGCGTTGCACCTCGCCGCGCAGAGCCTGCGGCTGGGCGAGAGCA
      >  R  G  P  S  L  S  I  D  T  A  C  S  A  S  L  V  A  L  H  L  A  A  Q  S  L  R  L  G  E  S
27298 CGCTGGCCCTCGCCGGCGGGGTCAACCTGATCGTCACGCCCGGGCAGTCGATCACCCTCGGCTCGGCCGGTGCCCTGGCACCCGACGGGCGC
      >T  L  A  L  A  G  G  V  N  L  I  V  T  P  G  Q  S  I  T  L  G  S  A  G  A  L  A  P  D  G  R
27390 AGCAAGTCCTTCGACGCCACCGCCGACGGCTACGGTCGTGGCGAGGGGTGCGGCGTCCTCGTGCTCAAGCTGCTCTCCGACGCCCAGCGGGA
      >  S  K  S  F  D  A  T  A  D  G  Y  G  R  G  E  G  C  G  V  L  V  L  K  L  L  S  D  A  Q  R  D
27482 CGGGGACCGGGTGCTGGCCGTGCTGCGGGGCAGCGCCGTCAACCAGGACGGCCGGACCAACGGGATCATGGCACCGTGCGGCCAGGCCCAGG
      >  G  D  R  V  L  A  V  L  R  G  S  A  V  N  Q  D  G  R  T  N  G  I  M  A  P  C  G  Q  A  Q
27574 AGCACGTGATGGTCCGCGCCCTGCGCTCGGCCGGCATCGAGGCCGGCAGCGTCGACTACATCGAGGCGCACGGCACCGGCACCCCGCTCGGT
      >E  H  V  M  V  R  A  L  R  S  A  G  I  E  A  G  S  V  D  Y  I  E  A  H  G  T  G  T  P  L  G
27666 GACCCGATGGAGGCCGCGGCGATCGGCTCGGTCTACGGGCAGGACCGCCCGGACGACGAGCCCTGCCTGATCGGTTCGGTCAAGTCCAACAT
      >  D  P  M  E  A  A  A  I  G  S  V  Y  G  Q  D  R  P  D  D  E  P  C  L  I  G  S  V  K  S  N  I
27758 CGGCCACCTGGAGGGCGCGGCCGGCGTCGCAGGCGTCATCAAGGCGGTCCTGGCGTTGAACCGGGCCGAGGTGCCCGCCACCCTGCTGGTCA
      >  G  H  L  E  G  A  A  G  V  A  G  V  I  K  A  V  L  A  L  N  R  A  E  V  P  A  T  L  L  V
27850 CCGAGGTCAACCCGGACATCGAGTGGAAGCGGCTGCGGCTGCGCCTGGTCACCCGCAACCAGCCCTGGCCGGACCGGCCGGGGCCGCGCCGC
      >T  E  V  N  P  D  I  E  W  K  R  L  R  L  R  L  V  T  R  N  Q  P  W  P  D  R  P  G  P  R  R
27942 GCCGGAGTCTCCGGCTTCGGCTACGGCGGCACCGTGGCGCACGTGGTGCTGGAACAGGCCCCGCCGGTCGCCGCCGAGCCGGCCCCCGGCGCT
      >  A  G  V  S  G  F  G  Y  G  G  T  V  A  H  V  V  L  E  Q  A  P  P  V  A  A  E  P  A  P  A  L
28034 GACCGGCGAGACGCTGTTCCCGATCTCCGCCGGCTCCGCGCACTCCCTTCGCGAGCGGGCCCGCGCCCTGGCCGGGATCGTCCCGGATGTCG
      >  T  G  E  T  L  F  P  I  S  A  G  S  A  H  S  L  R  E  R  A  R  A  L  A  G  I  V  P  D  V
28126 ACCTCGCCGCGCTCGGGCACACCCTGGCTCGGCGGCGTTCGCACCTGACCCACCGGGCGGTGGCGGTGGCCGCCGGCCGGGACGACCTGGTC
      >D  L  A  A  L  G  H  T  L  A  R  R  R  S  H  L  T  H  R  A  V  A  V  A  A  G  R  D  D  L  V
28218 GCGGCGGTTCGCGGCGCCTCGCCGACGACAGGCCGCACGACCGGGTGCGTACCGGAAGCCCGGTGGCGGAGCCGCCCCCACGGTGTGGGTGTT
      >  A  A  F  A  A  L  A  D  D  R  P  H  D  R  V  R  T  G  S  P  V  A  E  P  P  R  T  V  W  V  F
28310 CTCCGGGCACGGGTCGCAGTGGACGGGCATGGGCGGGAACTGCTGGCCACGGAGCCGGCCTTCGCGGACGCGATCGACCGCATCGAGCAGA
      >  S  G  H  G  S  Q  W  T  G  M  G  R  E  L  L  A  T  E  P  A  F  A  D  A  I  D  R  I  E  Q
28402 TCTTCCTCGACGAGATCGGTTTCTCACCCCGCCAGGCGATCCTCGACGGCGACTACGAGGCCGTCGACCGGACCCAGACAATGATCTTCGCG
      >I  F  L  D  E  I  G  F  S  P  R  Q  A  I  L  D  G  D  Y  E  A  V  D  R  T  Q  T  M  I  F  A
28494 ATGCAGCTCGGCCTGGCCGAGATGTGGCGAGCGAGGGGAGTCGAGCCGGACGCGGTGATCGGTCGGAGAGATCGCCGCGGCGGT
      >  M  Q  L  G  L  A  E  M  W  R  A  R  G  V  E  P  D  A  V  I  G  H  S  V  G  E  I  A  A  A  V
28586 GACCGCCGGCATCCTGACCGTGGCCGACGGCGCACGGCTGATCTGCCGTCGTTCCCTGCTGCTGCGCGAGGTCGCCGGCCAGGGCGCGATGG
      >  T  A  G  I  L  T  V  A  D  G  A  R  L  I  C  R  R  S  L  L  L  R  E  V  A  G  Q  G  A  M
28678 CCCTGGTGACGCTGCCCTTCGAGGAGGTCGCGGCCAGGCTGGCCGGCCGCGTCGACGTGGTCGCCGCGATCGCCTCCTCCCCCTCGTCGACC
      >A  L  V  T  L  P  F  E  E  V  A  A  R  L  A  G  R  V  D  V  V  A  A  I  A  S  S  P  S  S  T
28770 GTGGTCTCCGGCGACCCGGCCGCGCTGGACGCGCTGGTCGCCGAGTGGACCGAGGAGGGCCTGGGCGTACGCCGGGTCGCCTCCGACGTGGC
      >  V  V  S  G  D  P  A  A  L  D  A  L  V  A  E  W  T  E  E  G  L  G  V  R  R  V  A  S  D  V  A
28862 CTTCCACAGCCCGCACATGGATCCGCTGCTCGACCGGCTGCGCGCCGCCGTCGACTTCACCGCCCCGCGCACCCCGGGTGCCGATCTACAGCA
      >  F  H  S  P  H  M  D  P  L  L  D  R  L  R  A  A  V  D  F  T  A  R  A  P  R  V  P  I  Y  S
28954 CGGCGCTGGCCGACCCGCGGGCCCCGATCACCGCCGACGGCGAGTACTGGGCCGCGAATCTGCGCAACCCGGTCCGGCTCGCCGAGCGGTG
      >T  A  L  A  D  P  R  A  P  I  T  A  D  G  E  Y  W  A  A  N  L  R  N  P  V  R  L  A  A  V
29046 GCCGCCGCCGTCTCCGACGGACACCGGGCCTTCATCGAGGTCTCCCCGCACCCGGTGGTGACCCACTCGATCCACGAGACGCTGGCCGGAAG
      >  A  A  A  V  S  D  G  H  R  A  F  I  E  V  S  P  H  P  V  V  T  H  S  I  H  E  T  L  A  G  S
29138 CCTCGACGACGAGGTCTTCGTCGGCGGCACCCTGCGCCGCGACACCCCGGAGGCGCAGGCCTTCCTGTCCAGCCTGGGGGCCGCGCACTGCC
      >  L  D  D  E  V  F  V  G  G  T  L  R  R  D  T  P  E  A  Q  A  F  L  S  S  L  G  A  A  H  C
29230 ACGGGGTCGCGGTCGACTGGGGCCGGGTGCATCCGTCCGGGCCGCTGGTCACCCTGCCCGGCTACCCCTGGCGGCACCGGAGTCACTGGCAC
      >H  G  V  A  V  D  W  G  R  V  H  P  S  G  P  L  V  T  L  P  G  Y  P  W  R  H  R  S  H  W  H
29322 TGGCCGACGCCGGCCGCCGCCACGGGCCGGGGCCACGACCCCGCGTCGCACACCCTGCTCGGCGCGGTCGACAACGTGGCGGGCAGCGACGT
      >  W  P  T  P  A  A  A  T  G  R  G  H  D  P  A  S  H  T  L  L  G  A  V  D  N  V  A  G  S  D  V
29414 GCGGGTGTGGCGCACCGCACTCGACGACGCCAGCCGCCCCGTACCCGGGCAGCCACGCCCTCAACGGCGTGGAGATCGTTCCGGCGGCCGTGC
      >  R  V  W  R  T  A  L  D  D  A  S  R  P  Y  P  G  S  H  A  L  N  G  V  E  I  V  P  A  A  V
29506 TGGTGGAGACCCTCATGGCTGCCGCCGGGCGGGGCGACGGCCGCCCGCTGCTGACCGGCTTGTCGATGCGGTACCCGCTGATGACCGCCGGG
      >L  V  E  T  L  M  A  A  A  G  R  G  D  G  R  P  L  L  T  G  L  S  M  R  Y  P  L  M  T  A  G
29598 CTGCACGAGGTCCAGGTGGTGCGGGACGGTGCCGAGGTGCGGCTGGCGTCCCGTTCCGTCGACGCGGAGGCCGACCCGAGCCGGGACTGGCT
      >  L  H  E  V  Q  V  V  R  D  G  A  E  V  R  L  A  S  R  S  V  D  A  E  A  D  P  S  R  D  W  L
29690 GATCCACACCGATGCCACGGTGGCCGACGCCGACGCCACGGTGCTCGCCGCGCGGGCGTTGGCCGACCCCGACGACCACCGGATGGAACCGG
      >  I  H  T  D  A  T  V  A  D  A  D  A  T  V  L  A  A  R  A  L  A  D  P  D  D  H  R  M  E  P
29782 GCGACCCGGGCTCCATCCACCGCCGGCTCGCCGAGGTCGGGGTGCCGTCGACGGGATTCGACTGGTCGGTGGAGGAGCTGCTCTCCGGGTAC
      >G  D  P  G  S  I  H  R  R  L  A  E  V  G  V  P  S  T  G  F  D  W  S  V  E  E  L  L  S  G  Y
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Figure 11H

29674 GGCGTGCTCCGCGCGCGGGTGCGCTCGGCCGACTCGTCCACCTGGGCGCCGGTGCTGGACGCCGTCATGTCGGTCGCCCCCGCCGTCTTCCC
> G V L R A R V R S A D S S T W A P V L D A V M S V A P A V F P

29966 CGGCGTGCCGCAGCTACGCATGGTGGTGTACGTCGACGAGGTGCTGCTCACCGGCGAGCCACCGGAGGTGACGCTGATCGAGGTCGCCCTCG
>   G V P Q L R M V V Y V D E V L L T G E P P E V T L I E V A L

30058 ACCCAGACCGGCCCGACACGGCGAACGCGCTGGTCGCGGATGCTCAGGGCCGGGTCGTGGCCAGCCTTCCCGGGCTGCGCTACCCGGTGATC
>D P D R P D T A N A L V A D A Q G R V V A S L P G L R Y P V I

30150 GACCAGCCGGTCGCCCCGGCGCAGGACAGTTCCGGCGAGGTGGAGGAGGCGGTCTCCTTCGCCGGCCTGTCCGACGAGGAACTGCACGAGCG
> D Q P V A P A Q D S S G E V E E A V S F A G L S D E E L H E R

30242 GGTGTTCGACGAGGTGCGCCGGCAGATCGCCGGGGAGATGCGACTCGACGCCGACGACCTGCATCCCCGCCGGCCGCTGGCCGAGCAGGGCC
> V F D E V R R Q I A G E M R L D A D D L H P R R P L A E Q G

30334 TCGACTCGGTGATGACGGTGGTCATCCGGCGACGCCTGGAGAAGCGCACCGGGCGGAGCCTCTCCCCGACCGTCTTCTGGCAGCGCCCACC
>L D S V M T V V I R R R L E K R T G R S L S P T V F W Q R P T

30426 GTCGCCGCCATCGCCGACCACCTGGTGGAGCTGTTGAGCACCCCGCAGGAGTGAGGATCCGCGACGACAGGGAGGGCCCGTGCGTTCCGCA
> V A A I A D H L V E L L S T P Q E °

30517 CGGGCCCTCCCTGCTGTCGACGGATCTTCAGGTGGCGGGGTCAGCCCGGCCGCTGGTCCACCGCAGGGGTGGCGGCCCACTCCAGGTGGCG
                                            < ° G P R Q D V A P T A A W E L H R

30608 GCTCTCCCCGCAGGGTCTCCTCGGCGTTCTGTTCGACCCGCCGCATGGCGACGCGCCATGGCCGGCGCCATGACCGAGGTGACGACCGCGA
      < S E R L T E E A N Q E V R R M A V R L M P P A M V S T V V A V

30700 CCAGCACCACGATGGTGTATGAGGCGGTGTGTTCAGCACGCCCAGGCGCAGCCCGACCATCGCGATGATGATCTCCACGGCACCGCGCGCGTTG
      < L V V I T Y S A T N L V G L R L G V M A I I I E V A G R A N

30792 AGCCCGGCGCCGAGGGCGACGCCCTCCCAGTGGCTCTGCCGGGCCAGCCGTGCACCCAGGTACGCGCCGGTGTACTTGCCGAGCACGGCGAG
      <L G A G L A V G E W H S Q R A L R A G L Y A G T Y K G L V A L

30884 CGCCAGGATCACCGCCCCGGCGGCGAGCACCTCCGGGTCGGCGAGGGCACGCAGATCGACCCGGAGCCCCGCGCTGGCCAGGAAGATCGGGG
      < A L I V A G A A L V E P D A L A R L D V R L G A S A L F I P A

30976 CGAGCACGGACAGCACCACCGTGCGCAGCGGTGCCAGCCGGGCCGGCTCCCCGTTGCCGGGAAGGCCGATCAGGACACCCGCCACCAGCGCG
      < L V S L V V T R L P A L R A P E G N G P L G I L V G A V L A

31068 CCGAAGATCGCCTCCAGGCCCAGCGCGTGCGCCCCCGCCGCGAAGGCCAGCACGATCACCACGGCGACGGCGCTGGCGGCCCCGCCGTCGGG
      <G F I A E L G L A H A G A A F A L V I V V A V A S A A G G D P

31160 CTGGGCGTTCGCCCAGCGCATGGCGCGCCGGGTCACCGGCCGGCCGACCAGGACGGCCACCGCGAGGTAGGCCACGAGGTAAAGCAGGGCGG
      < Q A N A W R M A R R T V P R G V L V A V A L Y A V L Y L L A T

31252 TCACCACCTGCCCGGCGGTGAGGGTGCTCACCGCCACCGACGAGATGAGCGACAGCAGGAACCAGGCCGCAGCGTCCTCCAGCGACGCCGCA
      < V V Q G A T L T S V A V S S I L S L L F W A A A D E L S A A

31344 GCCAGGATGATCTGCCCCACGTCGCGGTTGCAGCAGGCGCATGTCGGTGAGCGTCTTCGCGATCACCGGCAGCGGCGTGACCGCCATCGCCAC
      <A L I I Q G V D R H L L R M D T L T K A I V P V A S V A M A V

31436 GCCGACGAACAGCGCGAAGACAGTCCGCTCCTGCCCGGCCGCGAGAAGCGCCGCCGGGGCCAGCAGGCCGGCGGCGATGCCCAGGCCGAGGG
      < G V F L A F V T R E Q G A A L L A A P A L L G A A I G L G L P

31528 GCACCGCGAGGCCGCCGACGGCCACCGCGCCGATCGTGCCGGCCCGCCGCCGGACCAGCCGCAGGTCCAGGTGCAGACCGGCCACGGCGACC
      < V A L G G V A V A G I T G A R R R V L R L D L H L G A V A V

31620 AGCAGTACGACGCCGAACTGACCGATGGCGTCGAGCAGGTGGACCTGGTCGGGGTCGGCGGGCAGCAGCCGTCCGATGTCGGGTGCCAG
      <L L V V G F Q G I A D L L H V Q D P D A P L L W R G I D P A L

31712 GGCCCCCAGCACCGAGGGGCCGAGCAGCACCCCGGTCAGCAGCTCACCGACCACCGCCGGCAGGCCGAAGCGTTGCGCCACCCGTCCCAGGA
      < A G L V S P G L L V G T L L E G V V A P L G F R Q A V R G L V

31804 CGACGGCGAGCAGCAGCAGCAGGCCCACCTGGAGCAGGAACAGCAGTAGCTGGTGGGAGCCCAGCGGGGGCACCGGCGCGGCCACGATCA
      < V A L L L L G V Q L L F L L L Q H S G L P P V

31894 CGGTCGTTGTTCCTTTCGTCTCGACGCCCGGCCGGGCCCGCCGGTGGTCAGGCCGCGATCTCGGGCGGCAGGTCCACCGGGTCGGCCGAGT
                                          < ° A A I E P P L D V P D A S N

31985 TCATGAAGGTCCGCAGGGCCCGCAGGTCGGCGGCGGGCTTCTCCCAGCCCAGCCCGGCGCACCAATCGATGAGGGAGGTCAGCTCCCCGGTG
      < M F T R L A R L D A A P K E W G L G A C W D I L S T L E G T

32077 GCCCGAACCTTGTCCTCCTCGGGCAGGCTGAGCACCGACATCTCGGCCGGCCACTGCACCACGTTGGCCAGGTCCACGTCGAGCCCCTCGGC
      <A R V K D E E P L S L V S M E A P W Q V V N A L D V D L G E A

32169 CCGGGCGAACTCCAGCAGGTCGCGCAGCCCCCAGACGTTGTCCCGCTGGGGTGCCACCTGGAGCCAGAGGTTGACCTCCGAGCGGGCCCGGC
      < R A F E L L D R L G W V N D R Q P A V Q L W L N V E S R A R R

32261 GGACGTTCGCGATGAAGGTCTCCCACTTCGCGCCCTGCCGGATCCGCTCGAACACCTCGCCGTAGCCGTCGCAGGAGGCGCCGATGCCGATG
      < V N A I F T E W K A G Q R I R E F V E G Y G D C S A G I G I

32353 CTCTTGAAGTGCCGGAACCGGTCGAAGACCGACTCCGGCAACACGGTGAGGTTGGAGTTGTAGACGACGTTGCCGGCGTTACCCGT
      <S K F H R F R D F V S E P L V T L N S N Y V V D V N G A N G T

32445 CTCCACCAGCAGGTCGAGCAGGGCGAAGTGGCCCGGCTGCATGAACGGCTCCCCACCGGCGAAGTACAGCCGCCGGATGAGGTGGGCGTTCT
      < E V L L D L L A F H G P Q M F P E G G A F Y L R R I L H A N E

32537 CGCGCAGGGTCTGCCACAGCTCGTCGTCGTCCCGGTAGGCGTCGATGACCGCGGACGACCAGGCCGGCCGCTTCTTGGCGCCCCAGCCCGAG
      < R L T Q W L E D D D R Y A D V A S S W A P R K K A G W G S

32629 CTGACCGGGTACGCGCACATCACGCACCGCAGGTTGCAGGTGTTGCCGAACCGGATGTCGAGGAAGAACGGGAAGTCCTCGACGGTGCCGTC
      <S V P Y A C M V C R L N C T N G F R I D L F F P F D E V T G D

32721 GGGCGCGGTGCGGGCGGCCAGCCGGTCGGGGTCGGCGATGTCCCGGAACCGCTGGTTGATCTCCTGCCGGTACGACAGCGCGCCGTGGTCCT
      < P A T R A A L R D P D A I D R F R Q N I E Q R Y S L A G H D E

32813 CGCGGTGGTAGCAGTAGGAGCAGTTCGTCGACCCGCTCCCCGGCCAGCATCCGCAGCCGGGTCCGGCGCATGTTGGGGCTGTTGAAGGCGTC
      < R H Y C Y S C A D V R E G A L M A L R T R R M

32904 CGCCAGGCCCATCACCCGGCCGGGGTTGTCCGCCGCGTAGCGGGACCGGCGCGAGCAGCCGACGGCGTCGTCGTTGAGCAGGAACTCCGGCT

32996 CCTCCTCCTGCTCGTACAGCTTGTTGTGGTACATCGAGTCGTCCACGCAGCACCGCCCGTAGACACCGTCGATGGACGCGCAGAGATGGATC

33088 CAGGGCAGCACGCACATGGTCCGGGACCGGGCTTCCGGGTCAGTCATGAAAGTTGATCACCTCGGTGGTGGGGGCGGTGTCATCCCGGTCG
                                                          < • G P R

33179 GCCGACCGTCTCGACCCGGGGCAGCGGGAAAGATCAACCGGGTGCCGCTGGCCAGCATCTCCGCCTCCCGGGCGACGATCTCGTCCCGGAAGT
      < G V T E V R P L P F I L R T G S A L M E A E R A V I E D R F H

33271 GCCAGGGCAGGACCAGGTAGTAGTCCGGGCGGGCCGCCCGCGACTCCTGCTCGCTGATGATTTCGATGTCCGTGCCGAGGGTGCGCGCGCCC
      < W P L V L Y Y D P R A A R S E Q E S I I E I D T G L T R A G

33363 ACCTTGTCCGGATTGCGCTCCGCGGCGTACCGGATGAGCTCGCGGTCTATGCCGCAGAACTGCAGGAGGGTGTTGCCCTTCGTCGACGCGCC
      <V K D P N R E A A Y R I L E R D I G C F Q L L T N G K T S A G

33455 GTAGACGTGCACCGTGCGGCCCCTGGCCCCGGAGCTCGCGCAGCAGGGCGCTCACCTCGTCACGGTGCTGGCGCACCTGCTCGGCGAAGCGCT
      < Y V H V T R G Q G R L E R L L A S V E D R H Q R V Q E A F R Q

Figure 11I

33547 GGTACGGGGCGTCGCCGTCCAGCCCCAGCGCCAGCTCCCGGTCGGCGAGTGCCTTGACCGAACCGTCGGCCCGGCCGCCCACCTCACCGGCC
     < Y P A D G D L G L A L E R D A L A K V S G D A R G G V E G A
33639 CGGGTGACCACGCAGCAGATCGAGCCGCCGTTCACCCCGTTGAGGCTGGCACGGACGATCTCCAGGCCCGCCGCGCCCAGAATGCGGCTCAG
     <R T V V C C I S G G N V G N L S A R V I E L G A A G L I R S L
33731 CGTGGCCAGCGAGTAGTAGGACAGGTGCTCGTGGCAGATGCTGTCGTAGCCGGCGATCTCCAGCATCGCCGGCAGGTAGGCGACCTCGACCA
     < T A L S Y Y S L H E H C I S D Y G A I E L M A P L Y A V E V V
33823 CCCAGACCCCGCCCGGGGCGAGCAGCGCCTCGACCTGACGGGCGAACTCCACCGGGTCCTCGACGTCGTAGAACATCGCGATCGAGGTGACC
     < W V G G P A L L A E V Q R A F E V P D E V D Y F M A I S T V
33915 AGGTCGAAGCTGCCCGCGTGCGGGACCAGCTCGGGGCTGGGGAAGAAGTCGCGGATCAGATTGAAGTCGTCGGGCGCGTCGTCGGCGGCGCT
     <L D F S G A H P V L E P S P F F D R I L N F D D P A D D A A S
34007 GGAGGGGTCGATGCCCCACCGCTGCGCGTCGGTCAGGTTGCCCAGCAGGGTGCCGTCGTTGCAGCCGATGTCGAGCACCTTGCCGGGCCGCT
     < S P D I G W R Q A D T L N G L L T G D N C G I D L V K G P R E
34099 CCCCCAACACCTCGACCGCCGCGTCCACGACGTCGGCGAGATGCCGGCGCATCGTGTCGTTGATCCGCGAGCGGTACCAGTAGGTGTCGTAG
     < G L V E V A A D V V D A L H R R M T D N I R S R Y W Y T D Y
34191 AGCAGCCCACCCGGCAGGGTGTGCCGCAACTGCACCAGGCCGCACGGGTCACCGCCGTCGCGTTCCGCGCACCGGGTCAGCTCCAGGGGGAA
     <L L G G P L T H R L Q V L G C P D G G D R E A C R T L E L P F
34283 GCGCACCCTGGGCGGGTCCGACACGCCGGGCTTCACGAAGCTGCCCTGTAGGTACTGGGCACCGAGGTCGAGGACCGTACGCAGGGTCCCGC
     < R V R P P D S V G P K V F S G Q L Y Q A G L D L V T R T G G
34375 CACACACCCGGCAGGTGGTCCGCTCGACCACCTCCGACGCCAACTCCTCGCCGGCCGCCGCCAACTGGCTCACGTCAGGTCCTCCTCGT
     < C V R C T T R E V V   < ∘ T R R T
34464 CTCGTGCCGGTGTGCGGGACCAGGCGCCCGTCGTGCCGGTTTGCTGGCGACCAGCAGGATGTCCAGATAGAAGGGCTGGTCGGGGCCCTCGC
     < E H R H A P G P A G D H P K S A V L L I D L Y F P Q D P G E S
34556 TGCGGCCGAGATGCCGGAACGCCCGGTCGAGGTACTCGTCGAGCGCGGCGGGCCGCAGCCGGTCCACCAGCCACAGGGCGGCGAGGGCCAGA
     < R G L H R F A R D L Y E D L A R P R L R D V L W L A R L A L
34648 CCCACCGGGCCGCCGGACGGCCAGCCGTGCTCGCGGCCGTACCAGCGCAGCAGCAGCAACAGGCCGCGCGGCCCGCAGGTCAGCTTGACGGT
     <G V P G G S P W G H E R G Y W R L L L L L L G R P G C T L K V T
34740 GCGGTCGACGGTGAAGCCGGCCCACTCGGCCTGGCGGGCCAGCCCGTCGGCGGTCCACCGCCACAGGTCCTGGCCGCCGTGCTCCTCCCACA
     < R D V T F G A W E A Q R A L G D A T W R W L D Q G G H E E W V
34832 CCCCGTGGGTGGAGAGCACCAGCCGGCCGCCCGGGCGCAGCAGCCGGTACGCTCCCGCAGGTACGCGTCCGCGTCCGAGACGTGTTCGAGC
     < G H T S L V L R G G P R L L R Y A E R L Y A D A D S V H E L
34924 ACCTGGGTGGAGAGCACCCCGTCGAACGTCCCGTCCGGCACCGGGCAGCGCCCGTCCCGGTCGAGGGCGTGGTCGGCCGGCAGGGACTCACC
     <V Q T S L V G D F T G D P V P C R G D R D L A H D A P L S E G
35016 GCCCGGGATGTCGGCGGTCTGCAACTCGGCGGAGCGGAACAGGCCCCGGTATGGCGAGGTGCCCGCCGTAGTCGAGCCAGACTCCCGTGG
     < G P I D A T Q L E A S R F L G R Y P S T G A G Y D L W G T A
35108 CGTCCCGGACCGCCTCCGCCAGCGCGTCGCGCAGGTCCAGGAAGTGGGCGTATGCCCAGTCCCCGGGCCGGGGCTCGATCCGCTCCCGGAAC
     < D R V A E A L A D R L D L F H A Y A W D G P R P E I R E R F
35200 CGTTCGGCCATCACCTCGTCCAGCGACGGGCCGGTGGGGGCGGTGCCGGCACCGGTCAGCAGGGGACCAAGCCCGGGTACGCGCCGCAGC
     <R E A M
35290 AGGGTCACCCAACGCCAGTACTCCTCGTGCGGGTACCGCATGGTGGTCGGCTCCGGCAGGCCCTCCCAGCGCCGCAGCGACGCGGCGGGCCG
        < ∘ W R W Y E E H P Y R M T T P E P L G E W R R L S A A P R
35381 GTACTCGAAGGGCTGCTCGCCGGCGTGCTCCGGTGCCGCCCGCCGCTGCGCCAGGCAGGAGAGCAGCACCTGCTGCTTGAGCCCGATGTACT
     < Y E F P Q E G A H E P A A R R Q A L C S L L V Q Q K L G I Y E
35473 CCGGCACGTGCGGGCCGAGGTCCAGCTCGACCTCGGCGGGCCGGTACTCGAAGTAGATGACCCGGCGCCGCTTGCCGGTCACCGCCGGCGCG
     < P V H P G L D L E V E A P R Y E F Y I V R R R K G T V A P A
35565 GCGTGCAGCATCAGGATGTTGTGCAGCATCACGTCGCCCGGGTTCATCACCGCCGGCACCGCCCCGGTGGTGTCCCACTCGGTGGCGTTCAT
     <A H L M L I N H L M V D G P N M V A P V A G T T D W E T A N M
35657 CCGGGTGGTGGTCTCGTTCGCCCGGTCGGTGTCCCAGTAGTTCGACTGCGGGATGCACCAGACGCAGTTGTCCTCGGGGCCGGGTCAAGGT
     < R T T T E N A R D T D W Y N S Q P I C W V C N D E P A P D L Y
35749 AGATGCCGACGTCGATCACCCGGCCCGCGCCGGTGATGCCGACCGCGTTCTCCGGGTAGGACCGCCGTCGCGGTGCCAGGGCAGCCGGGGC
     < I G V D I V R G A G T I G V A N E P Y L G G D R H W P L R P
35841 GCCCCCGCCTCGGTCTTGAAGACCATGCTGTCCCAGGTGGGGATGAGGTTGGGGCCGACCAGGTCCTCCATCGCCCGCAGCAGCAGGGGGTG
     <A G A E T K F V M S D W T P I L N P G V L D E M A R L L L P H
35933 GCCGGCGAGCCGGGCGACCACCGGGGACTTGTCGACCACGTACTCGATCCGCACCGGCGCCGCGTCCGGCTCGTGCGGTTCCAGCGTCCAGA
     < G A L R A V V P S K D V V Y E I R V P A A D P E H P E L T W I
36025 TGGTGTCGGTCATCGTCCGGGTGCGCCAGGCTTCGTCGATCAGCTGTCGGCCCGCCGCCTGCACGGACCGCAGCTCGTCGGGGTCCAGCAGC
     < T D T M T R T R W A E D I L E D A A A Q V S R L E D P L L
36117 CCGCGCAGGATCAGCGCGCCCTGCCGGCGGAAGGCGGTCAGGTGCTCCGGAAGCAGCCCGGTCTCGTGGATGTGGCACTCGGGGACGGCCTG
     <G R L I L A G Q R R F A T L H E P L L G T E H I H C E P V A Q
36209 CTCGGTGCGGACGTCCACAGTCGCGCTCATGGTTCGGTTCCCTTCTGCCAGGCGGACGGTTCGTGCTGCCCGGAGCCGCCGGCCGGGCCCG
     < E T R V D V T A S M
                    < ∘ P E T G K Q W A S P E H Q G S G G A P G P
36300 GGCTCGGTCGGTCGGCGACGAAGTACCAGTGCTCCCGCAGCGCGTCGGCGAACCCCGCCCGGTCCAGCGCCGGCTGCCCGGCGCGGCGCCCG
     < S P R D A V F Y W H E R L A D A F G A R D L A P Q G A R R G
36392 GGCAGGGTACGCAGCTCGTAACCCAGCTCGGTCACGAGCAGCGCCCACAGGTCGGCGCTGGTGGTGCCGTACTCCCGCATGGCGTGGTCGCC
     <P L T R L E Y G L E T V L L A W L D A S T T G Y E R M A H D G
36484 GCCGTGCTCGAAGACGATCACCGGCCGCCAGCGGCGGAGCAGCTCCACGGCACCGCGCAGGGCGAGCACCTCGCCGCCCTCGGTGTCCACCT
     < G H E F V I V P R W R R L L E V A G R L A L V E G G E T D V K
36576 TGACCAGGTCGATCCGGCGGTCACCGGGGAGCACGTCGTCCAGGCGGACGGTGTCGACCGTCAGCTCCCGCAGGGTCTCGTCCGGGCGGTCG
     < V L D I R R D G P L V D D L R V T D V T L E R L T E D P R D
36668 TAGGGACGCCGGCGCAGCCCGCTGTAGCCGGGGTTGGAGACCACGTGGACGAAGCTGTCCCGGCCGGTGCGCTCGGCGGCGGCGGCGGCCAC
     <Y P R R R L G S Y G P N S V V H V F S D R G T R E A A A A V
36760 CACCGTCACGCCGGGGAAGTCCCGGCGCAGCCCCTCGGCGTACGACGGCAGCGCCTCGACGGCCACGTGCGGCCACGGGGGGCGACCCGCA
     < V T V G P F D R R L G E A Y S P L A E V A V H R G R P A V R L
36852 GCAGGTGACGCAGGATGTCGCCGGCGCCGGCCCCGATGTCCACGGTGTTGGCGTCCGGTTCGCAGATCTGCTCGATCAGCGCCACGGTGAGC
     < L H R L I D G A G A G I D V T N A D P E C I Q E I L A V T L
36944 TGGTCGTACCAGTCGTTCATCGACAGCGCGCCGGCCTCGTCGGTCGCGGAAAGCTCAGTGGACATCGTCACGCTCCTCGGTCCGGCACGCC
                                           < • H V D D R E E T R C A
     <Q D Y W D N M

Figure 11J

```
37035 GGTCCGGCCCCGGAGCCGACCGCCGGGGCGGTACGGACCAGGAGTTCCAGCTCCCGCAGCTCGATCTCGGACAGCTCCAGGCCGGCGGCGCG
        <P  G  A  G  S  G  V  A  P  A  T  R  V  L  L  E  L  E  R  L  E  I  E  S  L  E  L  G  A  A  R
37127 GACGTTCTCCTCGACGACTCCGGGCGACTGAGCGCCGAACACCGGCACCACCCCGGCCGGGTGGTGCAGCGCCCAGGCCAGTGCCACCTGCG
        <V  N  E  E  V  V  G  P  S  Q  A  G  F  V  P  V  V  G  A  P  H  H  H  L  A  W  A  L  A  V  Q  A
37219 CGACGGTGTGCCCACGCTCGGCGGCGAAGGCGGCGAGGCCGTCGACCACGTCGAGCAGTTGGGCGTAGTCCTCACCCCGGAAGGCGTGCGAG
        < V  T  H  G  R  E  A  A  F  A  A  L  G  D  V  V  D  L  L  Q  A  Y  D  E  G  R  F  A  H  S
37311 TAGGCCCGCCAGTCCTCGGGGGCGAATGCCTGGTCGCGGTGCAGCGCGCCGGTGAGCAGCCCGTGGGCGAGCGCGGAGCCGCCCAGCACCCC
        <Y  A  R  W  D  E  P  A  F  A  Q  D  R  H  L  A  G  T  L  L  G  H  A  L  A  S  G  G  L  V  G
37403 GACGCCGGCCTCCTGGCAGCGGGGCAGCACCTCCTTCTCGGCACCACGGTCGAGCAGGTTGAACGGCACCTGGACGACGTCCAGCAGCCCGG
        < V  G  A  E  Q  C  R  P  L  V  E  K  E  A  G  R  D  L  L  N  F  P  V  Q  V  V  D  L  L  G  T
37495 TCGGCACCAGCTCGGCCAGGTCGCCCGACGTCACGTTGGCCGACATGCGGGCCAGGCCCTCGCGCACGAACCCCGCCAGCACCTCG
        < P  V  L  E  A  L  D  G  A  T  V  N  A  F  G  V  H  R  A  L  G  E  R  V  F  G  A  L  V  E
37587 GCGGTCTCCGCGAGCGGGACGGTCGGGTCGGGCCAGTGCACGGAGTACACGTCGACGTGGTCCGTGCCGAGCTGACGCAGGCTGGCCAGCAG
        <A  T  E  A  L  P  V  T  P  D  P  W  H  V  S  Y  V  D  V  H  D  T  G  L  Q  R  L  S  A  L  L
37679 CTCGTCCCGGAGGAACGCGGGGTCGCTGTTACGCACCGTCCGTCCGGGCGGGTCGAGCTTGTGCCGTCGCACGCCGGGCCGGGTCTCCAGCC
        < E  D  R  L  F  A  P  D  S  N  R  V  T  G  P  P  D  L  K  H  R  R  V  G  P  R  T  E  L  G
37771 CGCCGGCCGTGGCGATCACGATCTCGTCCCGGTGCGCGGGCAACAGGTCGGCCAGCCCGCGGGCAAGGGCCGCCTCGGCGGCCCCCGCCGCC
        < G  A  T  A  I  V  I  E  D  R  H  A  P  L  L  D  A  L  G  R  A  L  A  A  E  A  A  G  G  G
37863 TACGCCCGGGAGGTGTCGAAAAGGGTGACGCCCAGGTCGAAGGCCCGGCGGACGGCCTGCACGCCTGGTTCGATCCGCCGGCCCCACTGGCC
        <Y  A  R  S  T  D  F  L  T  V  G  L  D  F  A  R  R  V  A  Q  V  G  P  E  I  R  R  G  W  Q  G
37955 GCCGAGCGCCCAGGTGCCCAGGCCGAGCGCCGAGACCAGCGGCCCCCGCTCACCGATGCAGCGCTGCCGCACGGCGTCCTCCCGCCCGGTG
        < G  L  A  W  T  G  L  G  L  A  S  V  L  P  G  R  E  G  I  C  R  Q  R  V
38046 CCCCACCCACGCCCGTCGGCCGGCCGTCACGCGCCGGCTCCCGTCGCTGCGCAGCGTCAGGAACACCACGCCGTCGTGATTGATCATCT
                        < °  A  A  P  E  G  D  S  R  L  T  L  F  V  V  G  D  H  N  I  M  K
38137 TGTCGGTGACCGGCGTCAGCCCGGCCTCGGCGGCGATGCCGGTCATCAACTCCACGCCGTGCCAGTTCAGGAACCCCTTGAACTCCACGGGG
        < D  T  V  P  T  L  G  A  E  A  A  I  G  T  M  L  E  V  G  H  W  N  L  F  G  K  F  E  V  P
38229 TTCGGCGTCGGCGTACCGCTCGGCTAGGTGTGGAAGAAGCCGCGCGTGTTGTCGCGGAGGTCCAGGAAGTTGAAGCAGAACAGCCCGCCGG
        <N  A  D  R  Y  R  E  A  Y  T  H  F  F  G  R  T  N  D  L  D  L  F  N  F  C  F  L  G  G  P
38321 CCGCAGGATCCGCCGGATCTGACGGAAGTAGAGGAAGACCTCGAAGACGTTGAGGTGGATGAACACGTTCAGGGAGAACCCGGCGTCGAACG
        < R  L  I  R  R  I  Q  R  F  Y  L  F  V  E  F  V  N  L  H  I  F  V  N  L  S  F  G  A  D  F  A
38413 CGGCGGTCGGCAGCTTCTCCAGGAAGTCGTTCTCGATGTGGTGGTAGGAGACGTTCTCCCGGCCCTCGCAGGTGGCGCGCGCCTTGTCGAGG
        < A  T  P  L  K  E  L  F  D  N  E  I  H  H  Y  S  V  N  E  R  G  E  C  T  A  R  A  K  D  L
38505 AAGGATCGGCTGACGTCGGCGCAGAGCACGGCGCACCGGATCGGCGAGCCGGCCCATGATGCCCTCGCCGCTGCCGATCTCGAAGAT
        <F  S  R  S  V  D  A  C  L  V  A  R  V  R  D  A  L  G  A  A  M
38597 CTCCGATTCCGGGCCGAGCCCGAGCTGCTCGACGACCAGGGCGACCTTGTCGACACGGTCCTGGAGGTACTCCTCGCCGGCTGGTAGCCGG
38689 CGAGCTGCATCTGCATCTCCTCCGGCGTGTTCCACTCCCAGACGTAGTTGAGGTCGCCGGTGCTCCGGAGCGGACAGCCCCGGGGGGCGTCC
38781 TGCGGCGGCGGCGTCGCCTGCTTCGCGTCGTTCATCGGACCTCACTCGCGGTCTTGTCGGGCTCTGCGGGGACAACTGGGCGGGCGGCTGCG
38873 GAAAACTGGGCGGGCGGTGTCACGGACGCGCGGGCGAACTCCTGGGGCGACGTCCTCGGGGCTCAGCGCGGCCGGTGTCGGCCAGCCGGGCCAGGAG
                        < °  P  R  R  A  F  E  A  V  D  E  P  S  L  A  G  T  D  A  L  R  A  L  L
38964 TTCGGCCACCTGGACGGCGGTCGGCCCGGTGGTGACGGACTCCCGCATCCGCTGCGCCGCCACCCGGAATCGGTGGTCGTAGAGGACGGAGC
        < E  A  V  Q  V  A  T  P  G  T  T  V  S  E  R  M  R  Q  A  A  V  R  F  R  H  D  Y  L  V  S  G
39056 CGAGGGGCCTCGTCGACCTCCTCGCGGGACGCCTTCAGGCCGGGCAGCGTCTTCGTCGCGCCCTGCGGGTCGAGCCGCCGCCCGTAGATCAGG
        < L  A  E  D  V  E  E  R  S  A  K  L  G  P  L  T  K  T  A  G  Q  P  D  L  R  R  G  Y  I  L
39148 GCGTCGTAGTTGAGCGCCAGCGACAACTGCGGCAGCCCCATGGCGAGCCCGTTCATGTAGCAGTTGGCGCTGCCGTGGTGCACCAGCAAGTC
        <A  D  Y  N  L  A  L  S  L  Q  P  V  G  M  A  L  G  N  M  Y  C  N  A  S  G  H  H  V  L  L  D
39240 GCAGTCGGGGAGGATGAGCTCCAGCGGGCAGTTGCTGAGCACCCGCACGTTCGGCGGCAGCGCGCCCAGCCCCTCCACCTCGGAGGAGGCGG
        < C  D  P  L  I  L  E  L  P  C  N  S  L  V  R  V  N  P  P  L  A  G  L  G  E  V  E  S  S  A  A
39332 CGGTGATCACGACCTCCACGCCCCGCTGGGCGGCGGCGTCGACGGCGTGCCGCAGCGCCGGCACCTGCGCGCCGAACACGCCCGTGGCGGAG
        < T  I  V  V  E  V  G  R  Q  A  A  A  D  V  A  H  R  L  A  P  V  Q  A  G  F  V  G  T  A  S
39424 TTGCCCCACACCACGCAGACCCGCTTGCCCCGGCGCGGACCGAGCAGCCAGGGGTCCACGTCCTGGGAGCCGTTGTAGGGCTGGTAGCGGAT
        <N  G  W  V  V  C  V  R  K  G  R  R  P  G  L  L  W  P  D  V  D  Q  S  G  N  Y  P  Q  Y  R  I
39516 CGGGATCCGCAGCGCGTCGCCCATCGGCGGGATCGCCACGTCGGGCGACGGGTCGATGGCGTACCGGATCTGGTGCCGGCTCCACTCGACGC
        < P  I  R  L  A  D  G  M  P  P  I  A  V  D  P  S  P  D  I  A  Y  R  I  Q  H  R  S  W  E  V  G
39608 CGTACTTGCGGAACTCGGTCACGGGTCGCCGGAGACCAGGTCGAGCCCGGGCTCGGTCTCGATGGTGCCGATGAACCCGGGCGAGAAGTAG
        < Y  K  R  F  E  T  V  P  D  G  S  V  L  D  L  G  P  E  T  I  G  I  F  G  P  S  F  Y
39700 ACGCTGGGGATGTGGTGCAGCTCGGCGACCAGCGCGCCCTCCACGGCCATGATGTCGTGGACCACCAGGTCGGGCCGGTAGTGGGCGGCGTA
        <V  S  P  I  H  H  L  E  A  V  L  A  G  E  V  A  M  I  D  H  V  V  L  D  P  R  Y  H  A  A  Y
39792 GTCGACCGCGTTGTCGTAGCTGCGCTGGACCGCGGTGACCGTGCGCTTCCAGTAGTCGGCGAGCAGGTCGGTGTCGAAGTCGGCGAGCGAGT
        <D  V  A  N  D  Y  S  R  Q  V  A  T  V  T  R  K  W  Y  D  A  L  L  D  T  D  F  D  A  L  S  D
39884 CCATCGGCGGCCCGTGAAGGGGTTCAACGGCAGCGGTTGCTCCACCATGTGCTGCGGGGTGTAGAGGGCCTGGACGTAGAGCCCAGCCGG
        < M  P  R  G  T  F  P  N  L  P  L  P  Q  E  V  M  H  Q  P  T  Y  L  A  Q  V  Y  F  G  L  R
39976 GCGCTCTCCATCATGTCGGGTCCGTCGAGCACCGAGACGGGCATCATGCCCGCCGCGGCCACGCCCCGGACCTGGGACGGCGAACAGGCGAC
        <A  S  E  M  M  D  P  G  D  L  V  S  V  P  M  M  G  A  A  A  V  G  R  V  Q  S  P  S  C  A  V
40068 CTTGACGTCGTGGCCGGCCGCCCGCAGCGCCCAGGCCAGCGGCACCATGCACATGTAGTGCCCGGCCCAGTTGGACACGGTGAACAGAACCT
        < K  V  D  H  G  A  A  R  L  A  W  A  L  P  V  M  C  M  Y  H  G  A  W  N  S  V  T  F  L  V  K
40160 TCATCGCAGCCTCTCTGTGGCCTGCCGAGGGGGAGGTTGGGGGTCGCGGCCGGACGGTCAGGAGGTCAGGACCGGCAACTCCCGCGCGGGA
        < M                                              < °  S  T  L  V  P  L  E  R  A  P
40250 TCGGCGAACTCGATCACGATGGTGCGCCGCCACTGGTCGGAGGGGGTTCGGCCCGGAGCCGTGCACCAGCCGTACGTCGTGGACGATGAAGTC
        <D  A  F  E  I  V  I  T  R  R  W  Q  D  S  P  N  P  G  S  G  H  V  L  R  V  D  H  V  I  F  D
40342 CCCCTCCTGCGAGGGGACGGCGCACCCGCGGCCCGGCGTCGCGCACGCGTGACGTCGGCGTCGTCGGGCAGCAGGTGGGAGCCGGGCACGC
        < G  E  Q  S  P  V  P  V  R  P  G  A  D  R  V  A  T  V  D  A  D  D  P  L  L  H  S  G  P  V  G
40434 CCTCCAGACAGCCGTTCTCCGGCCCGGCGGTGTCCAGGCAGATGCTGATGTTGCAGACCGCGTGCGGGGGGACGTTGACCCGGTCCCGGTGC
        < E  L  C  G  N  E  P  G  A  T  D  L  C  I  S  I  N  C  V  A  H  P  P  V  N  V  R  D  R  H
40526 CACGGCACGCCGGCCGCCCGCAGTGGCTCCTTGAGCACCAACGCGAAGGCGGTGGGCACGACCGGGGTGCCGAGGACGTCGGCGGCCACCGC
        <W  P  V  G  A  A  R  L  P  E  K  L  V  L  A  F  A  T  P  V  V  P  T  G  L  V  D  A  A  V  A
40618 GGCGATCTCCGGCCGGTGCAGCAACTCGCCCTGCGGCCACGGCTCCTGCTTTTCGGAGGTTGTGGATCCAGGTACAGCACCGGCTCCGCCCTCGA
        < A  I  E  P  R  H  L  L  E  G  Q  P  W  D  Q  K  E  L  N  H  I  R  Y  L  V  P  E  A  G  E  V
40710 CCTCGTAGTTCCAGTAGTCGGCGTTGGCCCGCGCCGGACCGGCGAACCGGTCGATCAGGCTTACCGCGCCGGCCTTGAGCTGGGCCAGCACC
        < E  Y  N  W  Y  D  A  N  A  R  A  P  G  A  F  R  D  I  L  S  V  A  G  A  K  L  Q  A  L  V
```

Figure 11K

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40802 TCGGGGTCGAGCACCGGCCCGACGTGCGCGATCCCGTCGCTGCGGAACCGGCTGGCCACGGCCTCGCGCTCCCGCGACATGGTGGTCATCG
      <E  P  D  L  V  P  G  V  H  A  I  G  D  S  R  F  R  S  A  V  A  E  R  E  R  S  M  T  T  M
                                                                                       <  o  R
40893 GAGGCTCACCCCTTCGGTCGGTCGGCGCGTGCCGGTGCGGCGGCCGACGGCGATGATGTCGCACACCTCCGGCGACCGGCGCTCGTGCAGC
      <L  S  V  G  E  T  P  R  R  T  G  T  R  R  G  V  A  I  I  D  C  V  E  P  S  R  R  E  H  L
40984 ACCTCCACCTCGGCGAAGCCGGCGTTGTGCAGGCGGCGGAACAGGGACTCCCGGTCGAGCCAGCGCACGTCGACGCTGAGCCCCCGGGCCTG
      <V  E  V  E  A  F  G  A  N  H  L  A  A  F  L  S  E  R  D  L  W  R  V  D  V  S  L  G  R  A  Q
41076 CGGCTCGGGGTGCTCCTCGCGGACCTGCTTGACCGTGTAGCCGTCGATCGGTTGCAGGTCGCCCACGCCTCCCAGTAGTGGGTGGAGAGGT
      <P  E  P  H  E  E  R  V  Q  K  V  T  Y  G  D  I  P  Q  L  D  G  V  G  G  W  Y  H  T  S  L  Y
41168 AGATTCCCGCCGCGACGCCCGCGATGTCCTTCAGCAGGGTCCACGGCTCACGCACGTGGTAGAGCAGGCCCGCGCAGAGGACGGCGTCGAAC
      <I  G  A  A  V  G  A  I  D  K  L  L  T  W  P  E  R  V  H  Y  L  L  G  A  C  L  V  A  D  F
41260 TCGCCCAGCTCGGTGAAGTCGATCCGCTCCACGTCGGCGACGGCGCAGCTCCACGTTGGTGATGCCGTTGACCTCCATCACCAGCTCCGCGCG
      <E  G  L  E  T  F  D  I  R  E  V  D  A  V  R  L  E  V  N  T  I  G  N  V  E  M  V  L  E  A  R
41352 GCGCAGGTTCTCCGGACGGCCCTCCAGGGCAAGCACCGTCGTGCCGGGGTGCCGGGCGAGGGCAAGCGTGTCCGCGCCCTCCAGTGCGCCGA
      <R  L  N  E  P  R  G  E  L  A  L  V  T  T  G  P  H  R  A  L  A  L  T  D  A  G  E  L  A  G  L
41444 GTTCGAGGATCCGCCGCGCGTCGGGAAACGCACCGAAGAACTTCGCCGCCCGGTCGGCCGGGGACTGGCTCAGCAGATAACCGTGCTGGGAG
      <E  L  I  R  R  A  D  P  F  A  G  F  F  K  A  A  R  D  A  P  S  Q  S  L  L  Y  G  H  Q  S
41536 CCCTCGGCGTAACGCACTCCGTCGTGCTCGAATCCATTCACCCACGGCTCGAGCGCGGCGACGCGGCGACGAATCTCTTCACGGTCCATGG
      <G  E  A  Y  R  V  G  D  H  E  F  G  N  V
41627 GATCAAAGCCTAGCGATGCCATTGCGGTTGCGGACTAGTGTTTTCATCATATTCAGCGGCTCGCCGTGCTGAGCCTTTCGTTGACCAGCCG
                                 <  o  R  S  A  T  S  L  R  E  N  V  L  R
41718 GGCCCATTCCGGAATCCGGTCCCCGCCGATCTCGATATCGAAGGACGACTGGAGTTCCGCCGGCCCGGCGTCGGCCCGCCACCTGGCGGTGC
      <A  W  E  P  I  R  D  G  G  I  E  I  D  F  S  S  Q  L  E  A  P  G  A  D  A  A  W  R  A  T  R
41810 GGGCCAGTCCCTCGGCCAGCGGGGTGTCCGTCCAGTCGCCGAAGACCGATCGGGCCAGCTCCGTCGCGGTGTACGCGGTTCGCACCTCGTCC
      <A  L  G  E  A  L  P  T  D  T  W  D  G  F  V  S  R  A  L  E  T  A  T  Y  A  T  R  V  E  D
41902 CGCGACGGCAGGTGGGCGATCGGATGCTCCGGCACGCCGGCCGCCGACCGTACCGCCTGGGCCAGCTCCAGCACGGTGTTGGTGCTCGACGA
      <R  S  P  L  H  A  I  P  H  E  P  V  G  A  A  S  R  V  A  Q  A  L  E  L  V  T  N  T  S  S  S
41994 GCCCACGTTGAATGCCCGCCCCCACGCGGCCTCGGCTCTCGGCGGCGCGGCTGACCACGTTCACCACGTCACCGACGTACGTGAACGCGGA
      <G  V  N  F  A  R  G  W  A  A  E  T  E  A  A  R  S  V  V  N  V  V  D  G  V  Y  T  F  A  R  V
42086 CCTGGCCGCCGTCGCCGTACACGGTGATCGGCTCGCCTCGCAGGATCTGGTTGAAGAAGATGGCGACCGCGTTGCGGTACGGGTCCCGCATG
      <Q  G  G  D  G  Y  V  T  I  P  E  G  R  L  I  Q  N  F  F  I  A  V  A  N  R  Y  P  D  R  M
42178 TTCTGCCACTCGCCGTAGACGTTGTGCATGCGGAAGGCGGTGAAGGGCAGCCCCTGGGTCCGCATCGTCACCTCCAGCTCGCGCTCGACCAG
      <N  Q  W  E  G  Y  V  N  H  M  R  F  A  T  F  P  L  G  Q  T  R  M  T  V  E  L  E  R  E  V  L
42270 GTACTTGGCCAGGCCGTAGCTGTCCGCGGGGACGGGGACGGACTCGCCGCATCGGCGTCTCGCCGTGGCCGTAGACCGCCACGGAGGAGG
      <Y  K  A  L  G  Y  S  D  A  P  V  P  V  V  S  E  R  M  P  T  E  G  H  G  Y  V  A  V  S  S  A
42362 CGAAACAGAAGAACCGCACGCCGGTACGCAGCGACGCGTTGATCAGATTTATGCTGCCCATCACATTGGTGCCGTAGTTGAGCTGCTTCACC
      <F  C  F  F  R  V  G  T  R  L  S  A  N  I  L  N  I  S  G  M  V  N  T  G  Y  N  L  Q  K  V
42454 GAATGGCTGATCGCCTCCGCCGCGAAGGCGGCAAAGTGGAAGACCCGCTCGAATCGGTTCTCGGCGAACAGTGAATCGACGAAGTCCACGTC
      <S  H  S  I  A  E  A  F  A  A  F  H  F  V  R  E  F  R  N  E  A  F  L  S  D  V  F  D  V  D
42546 GGTCACCGAACCGACGGCCAGGTCCACCCCGGCCGGAACCCGCTGCCGGCTGCCGCCGCTGAGGTCGTCCAGAACGGTGACCCGGTGCCCAT
      <T  V  S  G  V  A  L  D  V  G  A  P  V  R  Q  R  S  G  G  S  L  D  D  L  V  T  V  R  H  G  N
42638 TCCTGACCAATGACTCCACCAGGTGCGAGCCGATGAATCCGGCACCACCAGTCACCAGACAACGAACCATCCGGGGCTCCTTCGTCAATA
      <R  V  L  S  E  V  L  H  S  G  I  F  G  A  G  G  T  V  L  C  R  V  M
42728 GATCCGGAAAGGGTTGACCGAGCGGGCGATCTGCGGCGCGCCCTTCGTCGGCGAACACCGACCCCCGAGAGAAAGCTTCGCCTCAGGGCAC
                                                                           <  o  P  V
42819 CGGCGACCGGTCGGCCTGCTTCTTCAGCGGCTCCCACCAGTCCCGGTGCGTCCGGTACCAGTCGATCGTCTCGGCCAGGCCGTCGGCGAAGG
      <P  S  R  D  A  Q  K  K  L  P  E  W  W  D  R  H  T  R  Y  W  D  I  T  E  A  L  G  D  A  F  A
42911 CGACCTCGGGCCGGTAGCCGAGCGCCCGCAGTTTCGCGTCCGTCAGCGAGTAGCGGCGGTCGTGGCCCTTGCGGTCCGGCACCCGCTCGACC
      <V  E  P  R  Y  G  L  A  R  L  K  A  D  T  L  S  Y  R  R  D  H  G  K  R  D  P  R  E  V
43003 CGGTCCCACCCGGCCCCCAAGGCGTCCAGCAGCGCGCCCGGTCAGCTCCATGTTGGACAGCTCAGCCGTGCCGGCGATGTGGTAGACCTCGCC
      <R  D  W  G  A  G  L  A  D  L  L  R  G  T  L  E  M  N  S  L  E  A  T  G  A  I  H  Y  V  E  G
43095 GGGGACACCGCGGTCGACGACGGTCTGGATGCCCCGGCAGTGGTCCGTCACGTGGATCCAGTCGCGGACGTTCCCGCCGTCGCCGTACAGCG
      <P  V  G  R  D  V  V  T  Q  I  G  R  C  H  D  T  V  H  I  W  D  R  V  N  G  G  D  G  Y  L  P
43187 GCACCCGTCGCCCGTTCAACAGCTCGGTGACGAACAGCGGGATCAGCTTCTCCGGAAACTGGTACGGCCCGTAGTTGTTGCCGCACCGGGTG
      <V  R  R  G  N  L  L  E  T  V  F  L  P  I  L  K  E  P  F  Q  Y  P  Y  N  N  G  C  R  T
43279 AGGCAGACCGGCAGCCCGTGGGTGCGGGCGTAGGCCAGGGCGATCAGGTCCCCGCCGGCCTTCGCCGCCGCGTACGGGGAGTTCGGCGCCAG
      <L  C  V  P  L  G  H  T  R  A  Y  A  L  A  I  L  D  G  G  A  K  A  A  A  Y  P  S  N  P  A  L
43371 GGGGGTGTCCTCGGCCCAGGAACCCTCGTCGATGCTGCCGTAGACCTCGTCGGTGGAGACCTGGACCACCCGGGCGACCCCGGCGTCGAGAC
      <P  T  D  E  A  W  S  G  E  D  I  S  G  Y  V  E  D  T  S  V  Q  V  V  R  A  V  G  A  D  L  C
43463 ACGCCTGCATGAGCGTCTGGACGCCCTGCACGTTGGTGCGGACGAACTCCGCCGAGTCGGCGATGACCGGTCGACGTGCGACTCGGCGGCG
      <A  Q  M  L  T  Q  V  G  Q  V  N  T  R  V  F  E  A  S  D  A  I  S  G  D  V  H  S  E  A
43555 AAGTTGACCACCACGTCGTGCCCGGGCAGCACCTCGGCCAGCAGCGCCGTGTCGCAGACGTCGCCCTGGACGAAGGTGATCCGGTCCTGGAC
      <F  N  V  V  V  D  H  G  P  L  V  E  A  L  L  A  T  D  C  V  D  G  Q  V  F  T  I  R  D  Q  V
43647 CGGTTCGAGGTTGGCGAGGTTGCCCGCGTACGTCAGCTTGTCCAGCACCGTCACCCGGGCCTGCGCCGTGTCGGGGTAGGCACCGGTGGCCA
      <P  E  L  N  A  L  N  G  A  Y  T  L  K  D  L  V  T  V  R  A  Q  A  T  D  P  Y  A  G  T  A  L
43739 GGTCGCGGACGTACTGCGAGCCGATGAAACCGGCACCGCCGGTGACCAGGACGCGACGCATCAGACCCCCACCCGGACTTCGCTGTGAT
      <D  R  V  Y  Q  S  G  I  F  G  A  G  G  T  V  L  V  R  R  M
                                                               <  o  V  G  V  R  V  E  S  H  D
43828 CGCCGAGGACGAACCGGTGCGTCTTGGGCACCCGGGGCCCGGGGACCACCCGCGCCTCCCGGCCGATCATCGAGAACTCGATGCGGCCGATG
      <G  L  V  F  R  H  T  K  P  V  R  P  G  P  V  V  R  A  E  R  G  I  M  S  F  E  I  R  G  I
43920 CCCTCGATGTAGGCACCGCGCAGCACGATGGAGTGCTCGATCTCGGTCTCCAGCAGGGTGCAGTCGCAGTCGATCGAGGTGTACGGGCCGAG
      <G  E  I  Y  A  G  R  L  V  I  S  H  E  I  E  T  E  L  L  T  C  D  C  D  I  S  T  Y  P  G  L
44012 GTAGGAGTTGCGGATGATCGAGCCGGCTCCGACCACCACCGGGCCGACGATCCGGGAGCCGCTGACGTCGGCGCCGGCGCTGATCACCACCG
      <Y  S  N  R  I  I  S  G  A  G  V  V  V  P  G  V  I  R  S  G  S  V  D  A  G  A  S  I  V  V  P
44104 GGCCGATCAGTTCGGTGCCGGTCGTCGACCTTGCCCTGCCGACCAAAGGCTCGACGCTGCCGAGGACGAACCGGTTCATCTCCAGCATGTCGGCG
      <G  I  L  E  T  R  D  D  V  K  G  E  V  L  P  E  V  S  G  L  V  F  R  N  M  E  L  M  D  A
44196 AGGTTGCCGGTGTCCTTCCAGTAGCCCGTGATCATGGTGGAGTCGACCCGGTGGCCGCGGTCGATCATCCACTGCACCGCGTCGGTGATCTC
      <L  N  G  T  D  K  W  Y  G  T  I  M  T  S  D  V  R  H  G  R  D  I  M  W  Q  V  A  D  T  I  E
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Figure 11L

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44288 CAGCTCGTTGCGCCAGGACGGCTTCAGCTCGGCCACGGCATCGTGGACCACCGGGCTGAAGACGTAGACCCCGACCAGGGCCAGGTCGCTCT
       <  L E N R W S P K L E A V A D H V V P S F V Y V G V L A L D - S K
44380 TGGGGTGCTCGGGCTTCTCCTCCACCCCGATCACCCGGCCGTCCGCGCCCATCTCGGCGACGCCGAAGGCGTGCGGGTCGGCGACCCGGGTC
       <  P H E P K E E V G I V R G D A G M E A V G F A H P D A V R T
44472 AGCATGATCTGCGCGTGCGGTCGCTCCTGCCGGAAGCGCTCGACGATGTCCTTGATCCCGCCGACGATGAAGTTGTCGCCGAGGTACATGAC
       < L M I Q A H P R E Q R F R E V I D K I G G V I F N D G L Y M V
44564 GAAGTCGTCGTCGCCGAGGTAGTCGCGGGGAGATGAGCACGGCGTGCGCGCAGCCCCCGGGGAGCCTCCTGCGGAAGGTAGGTCACCTGGAGGC
       <  F D D D G L Y D R S I L V A H A L G R P A E Q P L Y T V Q L G
44656 CGAACTGGGAACCATCGCCGACCACGCGCTGAATTTCGGGCGCGGTGCTGCCGACGACGATGCCCACCTCCTCGATACCGCCCTCACGAATA
       <  F Q S G D G V V R Q I E P A T S G V V I G V E E I G G E R I
44748 GCCTCGAGCCCGTAGAACAGCACCGGCTTGTTGGCCACGGGAATGAGTTGTTTGGCGGACGTGTGGGTGATCGGACGCAATCTCGATCCCAC
       <A E L G Y F L V P K N A V P I L Q K A S T H T I P R L R S G V
44840 CCCTCCCGCCAGGACCAGCGCCTTCACGAACGCCCTCGAAAGGATGGGACCGAGACGGGTCGCTGGTTCACGAGCACTCCAGGGGTCACGG
       <  G G A L V L A K V
44931 TGGACTGGGCTCTTCGTGAACGTACCGAAGGATCACTCGTGATTTCCCTACTTATGGGCCACCGAGGTGTGATCGGTGGATCTCTATGCGT
                                                                       < • A D
45022 CCGCCATTTCCGCAAACGGGGGCCTGGCCGGCCCGCCGCCGACCAGTTCGAGCACGGCGGCCAGGCCGTGCACGGTGTCCGGCGGGCTGGCC
       <  A M E A F P P R A P G G G V L E L V A A L G H V T D P P S A
45114 GGCAGCAGCAGGGTCTGCAGGCCGGCGTACACCGCCCCACCGTCGGCCAGGGTGTCGCCCACCATCAGCGCCCGCTCCGGGGCGACCTTCAG
       <P L L L T Q L G A Y V A G G D A L T D G V M L A R E P A V K L
45206 CTCGTCGCAGGCGGTGCGGAAGATCCGGGGATCGGGCTTGACCGCCCCCACCTCGTGGGAGAAGACGTAGGCGTCCACCAGCTCCGCCATCC
       <  E D C A T R F I R P D P K V A G V E H S F V Y A D V L E A M G
45298 CGTACGCCGCGAAGGTGGGCCGCAGGTCCCAGGCGATGTTGCTGACCACGGCGGTGCCCACGCCGCGGCGCAACTCCGCCAGGACCGGG
       <  Y A A F T P R L D W A I N S V V A T G V G R R R L E A L V P
45390 GCGGCGTCGCGGTAGGGCAGCCAGCCGTCCGTGCGGAACAGCCGGTCGTAGAGCGCCTCGGCGAGGCCGGGATGGGGCAGGTCGACGGTGGA
       <A A D R Y P L W G D T R F L R D Y L A E A L G P H P L D V T S
45482 GAGCAGGCCCACGTACGCCGCTGCGGTGCGTTTCGGGCGAGAGGTCCCGGCGGGCGTACACCTCGGCGAGCCCCGGCGGGACGGCGTGCGGCT
       <  L L G V Y A S R H T E P S L D R R A Y V E A L G P P V A H P E
45574 CCGGCCCGCCGGGACGGCCGGCCGCCAGCAGCAACCGGTCAGGGCCTCCTGCTGCGCCGGGTCGAGCTGGACGCCGACGGTGGCCGCCGCC
       <  P G G P R G A A L L L G T L A E Q Q A P D L Q V G V T A A A
45666 GCCCGCAGCCAACGCTGCGGCAGTTCCACGGCGAACAGCGTGCCGGAGAAGTCGAACAGGACGGCGTCGATCGGACGGGGCAGGGGGTCGT
       <A R L W R Q P L E V A F L T G S F D F L V A D I P R P L P T T
45758 CATCGCTCTCCTCGGTGCAGCCGCGTCAGGGCGGCACCAGCCTGGCAGCGGACCAGCCGGATGTCCATCATGGAGGAATGCGCCGGGTCG
       <  M
45848 GGCGCGCCCGCCATGGCCGCCGGTCCGGACGACAGGCATTTTCGGTCACTCTTGCCTTCTAGGCGGATTTCTTCAAAGATGGCTGTCAATTC
45940 TTCAGCGATCCTGGAGGCATCCGTGACCCGTACCCGAACCGCCCTGGGCCGGCTGCTCGCCGCCGGTCTGGCCAGCCTCGCCACCGCTGC
                               > V T R T R T A L R R R L L A A G L A S L A T A A
46030 CGCGACCCTCGTCGCCACCGCCGGCCCGGCGGCGGCCGCCACCACCCCCGGCATCGACGTGTCCCACTACCAGGGATCGATCAACTGGACGA
       >  A T L V A T A G P A A A A T T P G I D V S H Y Q G S I N W T
46122 GCGTCCGCAACGCGGGCATCCAGTTCGCGTTCATCAAGGCCACCGAGGGTACGAGCTACAAGGACCCCAACTTCAACGCCAACTACGTCAAC
       >S V R N A G I Q F A F I K A T E G T S Y K D P N F N A N Y V N
46214 TCCTACAACGCCGGAGTGATCCGGGGGGGCGTACCACTTCGCCCGGCCGAACATCTCCTCCGGCGCCACCCAGGCCAACTACCTGGCCAGCAA
       >  S Y N A G V I R G A Y H F A R P N I S S G A T Q A N Y L A S N
46306 CGGCGGCGCCTGGTCGGCGGACAGTCGCACCCTGCCGGCCGCCTGGACGTCGAGGCCAACCCGTACAGCGGCGGCACGTGCTACGGCCTCA
       >  G G A W S A D S R T L P A A L D V E A N P Y S G G T C Y G L
46398 GCACGTCCGGGATGCGTAGCTGGATCCAGGACTTCCTGAACACGTACAAGGCCCGCACCGGCCGGTACGCGGTCATCTACACCACCACGAGC
       >S T S G M R S W I Q D F L N T Y K A R T G R Y A V I Y T T T S
46490 TGGTGGAACCAGTGCACCGGTAGCTGGACCGGGCCGTGGGCCAACCACCCGCTGTGGCTCGCCCGCTGGTCGAGCACCCCGGGCACCCTGCC
       >  W W N Q C T G S W T G P W A N H P L W L A R W S S T P G T L P
46582 GGCCGGCGCTTCGGTCTGGAGCTTCTGGCAGTACACGGCCTCCGGCAGCGTCTCCGGGATCAGCGGCAACGTCGACCGCAACAACTGGAACG
       >  A G A S V W S F W Q Y T A S G S V S G I S G N V D R N N W N
46674 GCGACCGCACCCGGCTGATCGCGCTGGCGAACAACACCTGACCCGAACGCCCGGGTAGGCGGTTGGCGGCAGCGGAACCGATTGCGACCGT
       >G D R T R L I A L A N N T •
46765 ACGGTCGGCGGCCGGTCCGGCTGCCGCCAGCCGTCACCCGGCCCGCGTCGCGGGCCGCGCCGGCATCCGGTCCTGCCGGCCCGGGGTGGCC
46857 CGCCGTGCCATCCGCCAGGCGGCCACGCCTGCGACGGCGCCGGCCACGACACCGAACAGCGCGAACAGCACCGGAAGACCCGCGCTGACCAG
46949 CAGCAGCACCACGTCGCCGAAGGCGACGAGCATCCACAGTGCCAGCCCGGGTCGAGCGTCCCTGCGTCGGTGTCCCATGTCGCACCTCCTCG
47041 CATCGTCCGGGATCAGATACCCCGTTCGACGCAAGTACATGCGAATCGACATCGCAACGGCGGGAATCGCCTGCTCAGCGGGCCGAGTCGGC
47133 AATGGACGGCCCCGGCCGGGCGCTCAGTCGACCCGGTCCGGCTTGAAGCCCTTGGCGATCCGGTCGAAGTCGGCCAGCCGCGCCTGCCAGT
                                    < • D V R D P K F G K A I R D F D A L R A Q W D
47224 CCTTGTTCGCCACCTCCCACCGGAGGGCGTACCCCCGGTTGCTGGCCGTGACGAAGCCCCGGTTGCGGACGTGGATCCGAGTGCCGTCCCGG
       <  K N A V E W R L A Y G R N S A T V F G R N R V H I R T G D R
47316 TTCTCCAACCACTCCCAGTCCGCGCACGTCTTGTAGTAGTCGCAGCGCTTGATGCTCAGATACTGGTAGCCGTTGACGTAGTTCTTCCGGGC
       <N E L W E W D A C T K Y Y D C R K I S L Y Q Y G N V Y N K R A
47408 CGGTTCCTTCTCTTTCCAGTCGGCGTAGGCGTCGCCCTCCGGGGTGCTGGTCCACTGCACCAGCAGCTCGCCCACCCCGTCGCGCTCGTCGA
       <  P E K E W D A Y A D G E P T S T W Q V L L E G V G D R E D F
47500 AGACGATCGTGTTCTGCCCCACGCTGCGCCGCACCCAGCCCTTCGGCAGGGGCGAGCAGACCCGCCGGGTCCTTGTGCAGGAGCCAACCC
       <  V I T N Q G V S R R V W G K P L P L S F G A P D K H L L W G
47592 TCGGGCAGGGCGTTCGGGTCCACGGACGGGCTGGCAGACGGCGTCGGGCTGGGCGGAGCCGCGCTGCTGGTCGCCGGTGCGGCCGACGGCGT
       <E P L A N P D V S P S A S P T P S P P A A S S T A P A A S P T
47684 CGGCGTCGACACGCCCGCCTGCGGGTCGCCGCCGGGCCCCGGGTCGTCGTCACCGCTCCGGCCGGAGCAGCGGCACCGCCGCCAGCAGGCCGA
       < P T S V G A Q P D G G P G P D D D G S R G L L P V A A L L G I
47776 TCAGCAGCACCGCGACGAGCGCCGGACCAGCAGGCCGGCGGCGGACGCTCGGGCTTCGTGCCCCCGACGACGGTGGCCCGGCCCGTCGAC
       < L L V A V L A G V L L G R R R R E P K T G G V V T A R G T S
47868 GAGAGTGCCGGGCCGGAGGCGGCCGGCAGCACCGACGTCGGGGCGGCCTCCTCGCGGGGCGCGACGGCGGGCTCGCGGGCCGGGGCGGGCGG
       <S L A P G S A A P L V S T P A A E E R P A V A P E R A P A P P
47960 CGAAACGGACCGACGCCGCGCCCGGATCGACCCGGTGTCGTCGGCTCGGGTGTCGTCGGCCCGACCGGCCGCCGGGGCCCCGTCGGCCCCTT
       <S V P V A A G P D V R D D A R T D D A R G A A P A G D G A G E
48052 CGTCCCCAGCCTCGGCGGCCCGGTCCGCCGGCGGCCCGTCACTCCCTCCGGCCGGCGTGCCCGCAGCCTCGTCGGCGCTGGTCGCGGCGTCG
       < D G A E A A R D A P P G D S G G A P T G A A E D A S T A A D
```

Figure 11M

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48144 GGGGCGGGGATCTTCGCGGTGGGATCGGCCGCCTGCGGGCCGAAGTCGGTGACCTTCGCGGTCGGATCGGCGTCGGCGCTCGGCAGGTCGAC
        <P  A  P  I  K  A  T  P  D  A  A  Q  P  G  F  D  T  V  K  A  T  P  D  A  D  A  S  P  L  D  V
48236 CATCGCGGTCGGCGCGGCGTCCACCCCCGCCGGGACCTTCGCGGTCGCGTCGCCGCCGCCCACGCCGGCCGCCGCCGCGCCACCGGCGGCAA
        <M  A  T  P  A  A  D  V  G  A  P  V  K  A  T  A  D  G  G  G  V  G  A  A  A  A  G  G  A  A  L
48328 GACCACCTTCCGGGGTACGCGGTGCGGGCGGGGCCGCCGGCCGGCCGGTGCGCTGTTCGGCGGGGCGCGGTGCGGGCACCACCGGCGGTCGC
        <  G  G  E  P  T  R  P  A  P  P  A  A  P  R  G  T  R  Q  E  A  P  R  P  A  P  V  V  P  P  R
48420 GGCTCGCGCGGGCCGTTCGGCCCCGGCCGGCGTACGCCGTCGAGCAGCGAGATGGTCTTGGCGCGACGCCCGGCGGCCCGCAGGAGCCG
        <P  E  R  P  G  N  P  G  P  R  R  V  G  D  L  L  S  I  T  K  A  R  R  G  A  A  R  R  L  L  R
48512 CTCGGCCACCTCGGCGTCGATCCGCTCGGCCGGGTCCTTGCGGAGCAGCCCGTTCAGCACCGGCTTCAACGGGCCGGCGTTCCTCGGCGGCG
        <  E  A  V  E  A  D  I  R  E  A  P  D  K  R  L  L  G  N  L  V  P  K  L  P  G  A  N  R  P  P  P
48604 GCATCGGCTCGGTGGCCAGCGCCGCCAGGGTGGCGATCGCCGACGGTCGGGCGAACGGCGACTTGCCCTCCACCGCCGCGTAGAGCGTCGCG
        <  M  P  E  T  A  L  A  A  L  T  A  I  A  S  P  R  A  F  P  S  K  G  E  V  A  A  Y  L  T  A
48696 CCCAGCGACCAGAGGTCCGCCTCCGGGCCGGCGGTGCCGTCCCGCGCCCGCTCCGGGGCGATGTACGCCGGGGAGCCCAGCACCATTCCGGT
        <G  L  S  W  L  D  A  E  P  G  A  T  G  D  R  A  R  E  P  A  I  Y  A  P  S  G  L  V  M  G  T
48788 CCGCGTCACGTTCGGGTCACCGGGGATGGTCGCCAGGCCGAAATCGGTCAGCACCACCCGGCCGTCGGTGCCGAGCAGCACGTTGCCCGGCT
        <  R  T  V  N  P  D  G  P  I  T  A  L  G  F  D  T  L  V  V  R  G  D  T  G  L  L  V  N  G  P  K
48880 TGATGTCCCGGTGCATGACGCCGGCCTTGTGCGCCGCCTTCAGCGCGCCGAGCACCCCCAGGCCGATCTCGACCGCCTTGGCCGGCGACACC
        <  I  D  R  H  M  V  G  A  K  H  A  A  K  L  A  G  L  V  G  L  G  I  E  V  A  K  A  P  S  V
48972 GGCCCGTCCTCCGCGAGAGTGTCCTGAAGGGACTTCGACGCCACGTACTCCATGACGATCCACGGGTCGCCGTCGGTGCGCAGAACGTCGAA
        <P  G  D  E  A  L  T  D  Q  L  S  K  S  A  V  Y  E  M  V  I  W  P  D  G  D  T  R  L  V  D  F
49064 GATGCGGACCACGTTGACGTGGTTGAGTCGCGCGATGGCACGGGCCTCCCGCAGCGAGCGTTCCCGCATCTCGCGGCGCTCCTCCGGGGTGA
        <  I  R  V  V  N  V  H  N  L  R  A  I  A  R  A  E  R  L  S  R  E  R  M  E_ R  R  E  E  P  T  L
49156 GGCTGGGCGGCGGGACCAGTTCCTTGATCGCCACATCCCGGTGCAGCACCTCGTCGCGACCTTCCATACCCGACCCATGCCACCCTGACC
        <  S  P  P  P  V  L  E  K  I  A  V  D  R  H  L  V  E  D  R  A  K  W  V  R  G  M
49247 GAGCGGCGAAATCAGCCGGTACCGGTCGGCAACGAGTTGGGGAAGCGCGTTCGACATCGGTGGAGACGGTACCGGCGGCGGCCCGCCGCAC
49339 ACCGCCGGCACGCCACTGTGCGACGAAGGTCAAGTTCGCGACGCGTACGCTGAACGGCATGTCTGCCGAAGAGCCGCTGTTCCGGGTGACCC
49431 GGGGCGTTCCGACCGCCGAGGAACTGGCCGCGCTGGTCGGCGTCATCGTCGCCCGGACCCGCTCCGCCGCCGCTCACGCGCCCGCCGCGCCG
49523 TCGGCCTGGGCACGCAGCGGTCGACGAGTACGGTGCTCGCCGCTCGCCCGGGAGCCTGGCGCGCCTCCGGTCTGCCCCGCTGACGCAC
49615 TCGCCAGCATGTGGCCAGTGTGGCCCGCCGCCGAGGCGGGTGGCGGCGGGGGCTCCCGGAGGTCGACGACACCCGTTAACCTCACTCAGGGA
49707 GACGATGCCGTGACGGATAGGGAGGGTCGATGATTCCCGAGGAGGACCGACCAGCACCCTGGTTGAGCGGCTACGGCAGCATCGAGGCCGAC
49799 ATCCGCCAGATGCGCGAGTTCGCCGACAAACTCCAGGCGGAGGTCGAGCGGAACTACGCACCGCATCTGTCGTACATAGCGGACGACATGAA
49891 GGCACAGATCCCCAACCCCGCCGACGCCTTCGTCGAACTGGTGCAGTTCCTCAAGGCGCACAACGAGACCCAGCAGGCCACCGCCACGATGG
49983 TCTTCCGTCGGTGGGGGCCACCGGCCCACCTGGCCACGGCAGCCGGCCGGATCGCCGAGCAGTACGCCGACTCCGACGCCTTCTCCGCCGCT
50075 CGCGTCTCCGACGTGGAGCGGGCCCTCGCCAACCCGGCGCGGCGGGGCAGGGCCGCCCCACGCCGGCTCTGCCCGACCCGACCAGCCCGGA
50167 CGGCGGGCGCGGGGCGGGTGGTGCTGCCCATGATCGAGCGGGGCAGCGGCGGACGTCCGGCCTCACCGACTGGCGGCTGATGGACCTGCTGAG
50259 CATGTGGGCGTGCATCCAGGACCACGAGACCGCCGGGCACTGGAAGCAGGTCGCCGGCTGGCGCAAGGTTTGCGACCTCGCGCAGGCCCACC
50351 TGGGCCGCCTCAAGGAGTACCGGCGCGGCCTGGCCGAGGCGTGGCCACCGGCGACCAACGCCGCCGCCCGGGCGTACCTCGGCGAACTGGAC
50443 GACCTGATCGACAAGGTGCAACGCACCCACGACGCGGCTGCCGCGAACTACGACGCCCTCGCGGCCGCCACCCGAGCGATCAGCAGCGCCCG
50535 CACCGAACCTCAAGCCGCTACACGAGTACGTGGAGAAACTCCAGACAGAAGCGGGCGTACGAGGCGACTACCGCGATCCGAAGGCGCTGA
50627 TGGGCAGCCGGCTGCCGGACAAGCCGGTGACTGACGCCGACCTGGAACGACTCAACGCCCAGGCCCGGAACCTGATGTACGGGTTGAGCGGC
50719 GAACTCCAACAGGCCCAAGCAATGCTCCGCCAACCCCCTCCTCCGCACCGCCCAGGACGACAGCCGAACAACCCGGATGCTTACGAGAGCAC
50811 AGGCACGCCTCCGGTCATCCCGCCCGTATTACCAGTCCCAACCATTAGGCCTTCAATTCCCTCAAGCGCTCAGCAAGCAGAGCCACGCCCTG
50903 TTCCTGTCCAGAGCGCACCCCAAACAGGTCCTGTACTCGGGGGAATCGGGACGGGAAACACCACTTCGCCATCGGGCTCCATTTCTCCCGGC
50995 ACCGGCCACCCAGTGACATCCAACCCGGCAGGAGGTGCTGGCCCTACCCTCCCGCCGAACTTGCCACCTGCCATCGCCCCCACTGGACGAGG
                                                                          junction marker
51087 CAGCACAACCGGCCAGGTAGGAAACCAGCCCCGCTCAACCACGTCCTCACGACCATTCTTGCCAGGCGGCCTGATCGGCGGCGGGCCCGCGA
51179 TGGGGATTAATCAACCCCTTGGCAATACTCCTCCGCGAAGGATCAACCCAATTGGAGGGGTGATCGGGGGCGGTGGGGCTGGAACCTCACCA
51271 ACCGGCGCTGCAGGCACTCGCCCGGGCTCGGGACGTGGTCCCCACTTTAACCTGACCCCTGCGGCGCCTCCGAATGGCGCACCGCAAGGCGT
51363 CGTAAACACCTTAGGTCTGAATGGTGAGCCGTCACGCTCATCCCACCGCGAGCAAGGCGATACTGACGGCCGCTACTGGGATCCCGACCATC
51455 CATGGGCAACCAGCGAGGGCGTTCCTCCAGTAGTCCGCCCGCCCGAGGCGGAGGGACCAATCGACCCAGGGCCAGCTATTGGCTTCGACCGG
51547 TGAAAAACGCTCCTCCAGCGGGCGCTACCTTCACCTTCCTAGCAACATTGATGGTTGCATCAGCGTACGCCCCGAGCGCCGTGCGTGCGA
                                                                                       >  V  R  A
51637 GTCCTGAAACCGATGGTGCCTTGCGAATACGGGCTGACCAGTGGCACCTTAACTACCTGAAGGCGGCGGAGGCTCAGAAGCTGTCACTGGGA
        >S  P  E  T  D  G  A  L  R  I  R  A  D  Q  W  H  L  N  Y  L  K  A  A  E  A  Q  K  L  S  L  G
51729 GAAGGGGTTGTAGTAGCGGTCCCCGGATACTGGCGTTGATCCACACCCCGACCTTCAGCGCAATCTAATCAAAGGGATTGACATCATTCCCGG
        >  E  G  V  V  V  A  V  P  D  L  Q  R  N  L  I  K  G  I  D  I  I  P  G
51821 GGGCAATGGAGATGGCCAGAAAGATCGCAACAGTCACGGCACTAGCATGGCTGGCTAATCGCAGCCCACGGACAGGGCCAGAGCGGCGCCT
        >  G  N  G  D  G  Q  K  D  R  N  S  H  G  T  S  M  A  G  L  I  A  A  H  G  Q  G  Q  S  G  A
51913 TAGGCATAGCACCCAGAGCCAAGATCATGCCAATCCTGTCTTCCGCGTCGAACAACCTCGGTGATGCAGACGGCTTGGCTGCGGGTATAGAA
        >L  G  I  A  P  R  A  K  I  M  P  I  L  S  S  A  S  N  N  L  G  D  A  D  G  L  A  A  G  I  E
52005 TTTGCAATCTCGCATGGGGCGGATGTCATCAATGTCTCCAGCGGAGGCGGCGCCAGCGTTCATCATCAAGGCAATCAGAGAGGCGGTCGC
        >  F  A  I  S  H  G  A  D  V  I  N  V  S  S  G  G  G  A  S  V  R  L  I  K  A  I  R  E  A  V  A
52097 CGGCAGACATTGTAGTTGTCGGCAGCCGCCGGAAACAGTCCCGAAGACATGACAATTGGCTATCCAGCCAGCGAGGAAGGAGTCGTCGCAGTTG
        >  A  D  I  V  V  V  A  A  A  G  N  S  P  E  D  M  T  I  G  Y  P  A  S  E  E  G  V  V  A  V
52189 GCGGAATTGATCGACAGGGAGAGCATGCTTCAGTTTCTGTCGTCGGACCGGAAGTTGACTTAGTCGCACCGGCAGTCGACATCTACAGCACC
        >G  G  I  D  R  Q  G  E  H  A  S  V  S  V  V  G  P  E  V  D  L  V  A  P  A  V  D  I  Y  S  T

52281 AGTTACGACGGGAAGTACTCCAAAGGCACCGGTACGTCCAGTGCCACAGCGATAGTCGCAGGGGCCGCTGCTCTGGTCCGATCGAAGTTTCC
        >  S  Y  D  G  K  Y  S  K  G  T  G  T  S  S  A  T  A  I  V  A  G  A  A  A  L  V  R  S  K  F  P
52373 CGACCTGCCCGCCTCGGAGGTCGTCCATCGCCTCACTGCCACCGCCATCGACAAAGGGCCGCCAGGGCACGACGACCAGTACGGCTACGGCG
        >  D  L  P  A  S  E  V  V  H  R  L  T  A  T  A  I  D  K  G  P  P  G  H  D  D  Q  Y  G  Y  G
52465 TTATCGACCTGGTTGCCGCGCTTACGGCAGACGTATACCCCGGGTGGGCTTTGAGTCGGCGGACGGGACGTGCCCGACGTGCCTGGGTGACC
        >V  I  D  L  V  A  A  L  T  A  D  V  P  P  V  G  F  E  S  A  T  A  D  V  P  T  V  P  G  S  T
52557 ACGACGGCGGTCGCCGAGCCGGCAGGCGAGGGTGACGATGGGCAACGGCCCGAGGTCTGGCCACGTTGGGAGTGATCGTGGCTGCTGCGGG
        >  T  T  A  V  A  E  P  A  G  E  G  D  D  G  A  T  A  R  G  L  A  T  L  G  V  I  V  A  A  A  G
52649 CGCTTGGGCGCTGGTCGCTCGACGGCGTAGGTTGAGCGACGACCCGCCCCCGCGGATCAGCCGGTGACCAGCCAGCCCTGACGCCATGTCG
        >  A  W  A  L  V  A  R  R  R  R  L  S  D  D  P  P  P  R  I  S  R  •
52740 GCGACATTGGGGGGTCGGGGTGGGTGGGATACCGCTATTTGGCCGACATGAAGTCGATCAACAGCGATCAACAGGCAGTGTGATCGGCGGGG
```

Figure 11N

```
52832 GTCGGTCGACGGCCAGGCGGCGTCGACGGAGGCGGGGGAAGCGGTAGCGTCGGCGACGTGCCGAACTCGATTTCACTCCGACTCGTGCTCGC
                                                          > V P N S I S L R L V L A
52924 GTCGGCGAGCCCTGCCCGTCGCAAGCTCCTCCACGCCGCCGGCATCGAACCCGACGTGCTGGTCAGTGGGGTCGACGAGTCCCAGGTGACCA
        > S A S P A R R K L L H A A G I E P D V L V S G V D E S Q V T
53016 GCGAGCGAGCCGAGGATCTGTGCCTGGAGCTGGCCCGCCTGAAGGCGCAGGCGGTCGTCGGCCGGCTGCGCCCGTCGGCCGACGAGCGGACG
       >S E R A E D L C L E L A R L K A Q A V V G R L R P S A D E R T
53108 CTGGTGCTCGGCTGCGACTCGGTGCTCGCCTTCGACCGCGAGATTCTCGGCAAGCCGGCCGACGAGGCGGACGCTACCCGGCGTTGGGAGCG
        > L V L G C D S V L A F D R E I L G K P A D E A D A T R R W E R
53200 GATGCGGGGGCGCAGCGGGGTGCTACACACCGGGCACTGCCTGATCGACGTCATCCACGAGACGCGCGCCGAGGCGGTCGCCTCGACCACCG
        > M R G R S G V L H T G H C L I D V I H E T R A E A V A S T T
53292 TGCGTTTCGCTGACATCAGCGACGAGGAGATTGCCGCGTACGTCGCGACGGGCGAACCGCTCGGTGCGCCGGCGCGTTCACCATCGACGGA
        >V R F A D I S D E E I A A Y V A T G E P L A V A G A F T I D G
53384 ATGGGCGGGGCGTTCCTGGAGGGTGTCGACGGCGACCCGGGCACGGTGGTCGGCCTCTCCCTACCGTTGCTGCGCCGGCTTCTCGGCGAGCT
        > M G G A F L E G V D G D P G T V V G L S L P L L R R L L G E L
                                                                           > M T T K
53476 GGACCTGCGGATCATCGACCTGTGGACGAAGGTCGCGCCCGGGCGGCCAGGCGGTCGAGGCGGTGGGTACGGTCCAGCCATGACGACGAAGT
        > D L R I I D L W T K V A P G G Q A V E A V G T V Q P •
53567 CCCTGCCGCTGACCCCGGAACTGCATCGTACGTGGTGGCCCACGGATCGGACCCGGACGAGGTGATGCGGGATCTGATCGAGGAGACCCTC
        >S L P L T P E L H A Y V V A H G S D P D E V M R D L I E E T L
53659 GCCGCGCTGCCCGCCGAGGCGAGGATGCAGGTGGCCCCGGAGCAAGCCGCGTTCCTGACGTTCCTCACCCGGTTGATCGGGGCGCGGCGGGC
        > A A L P A E A R M Q V A P E Q A A F L T F L T R L I G A R R A
53751 GGTGGAGGTGGGCACCTTCACCGGCCTGTCCTCCCTGGCGATCGCGCGGGCTGGCCGAGGGCGGGCGGTGACCTGCTTCGACATCTCGG
        > V E V G T F T G L S S L A I A R G L A E G G R L T C F D I S
53843 AGGAGTACACGGGCGTCGCGCGGCGGTACTGGGCGCGGGCCGGGGTGGCCGACCAGATCGACCTGCGGATCGGGCCGCCGGGGACACGCTG
        >E E Y T G V A R R Y W A R A G V A D Q I D L R I G P A G D T L
53935 CGCGGGGTTGCCGTACGAACGGCACCTGGACTTCGCGTTCATCGACGCGGACAAGGTCGGCTACCCGGTCTACTGGGCGGAGTTGGTGCCCG
        > R G L P Y E R H L D F A F I D A D K V G Y P V Y W A E L V P R
54027 CATGCTCCCGGGCGGGGTCATCGCGTGGACAACACGTTGCGCGGGGGCCGGGTGCTCGCCCGCGTGACGACGACCGGGCCATCGCCG
        > M L P G G V I A V D N T L R G G R V L A P R D A D D R A I A
54119 CGTTCAACGACGAGGTGATGGCCGACGTCCGGGTGGAGCCGGTGCTGCTGCCGATCGCCGACGGGCTGACCCTGGCCCGGGTGCGCTGACG
        >A F N D E V M A D V R V E P V L L P I A D G L T L A R V R •
54210 GGCGCCAGCCGGACGATCGTGCCAGGTCGCCGGCCCGGCGTCGTGTGTCCGCCTCACCGGGTCGACGAGGGGGTGAGGCGGGGCGGGGTGTT
54302 AGGAAGGGGCCCTTCCTATACCGAATGCGTTAACAAGGGGCCCCTCCTTACACCTCAACCTCAGCGCACGCTGCCGGCGAACTGGCGGGCG
                                                         < • R V S R A F Q R A
54393 GCCCAGGCGACGCCGACGGCGGCAAGCACCGCGATGATGGTCAGGCCCTGCCAGACCTTGTCGTTGCCGAGGTCGCCGGCGAAGAGGGCCCG
       <A W A V G V A A L V A I I T L G Q W V K D N G L D G A F L A R
54485 GGTGCCGTCCACGGCCCAGGAGAACGGGTTCCACTCGGCGATGCGCTGGAGCCAGCCGGGGGCGAAGGTGAGCGGCAGCAGGATGCCGGAGA
       < T G D V A W S F P N W E A I R Q L W G P A F T L P L L I G S L
54577 GCAGCAGCACCGGCTGGGCGACGGTGTTCATCGGGGCGAGCGCGTCCTCACTCTTGACCTTGAGCGCGACGCCGTACGACGGCCGAG
       < L L V P Q A V T N M V P A L A D E S K V K L A V G Y S V A S
54669 GTCATCAGCGCGATCAGGGCGAGCATCAGGTACGCCAGCAGCAGGTCGCCGATGAACACGCGCAGCTCGAACAGGAGCGCGAGCAGGGTGAT
       <T M L A I L A L M L Y A L L L D G I F V R L E F L L A L L T I
54761 GATGACGGCCTGGGCGAGCAGCGACACGACGTCGCGCAGGGCCCGGCCGAGCAGCAGCGCGAGCCGGCTGACCGGGGTGACCCGGGACCGTT
       < I V A Q A L L S V V D R L A R G L L L L A L R S V P T V R S R E
54853 CGATGACGCCGGCGCGCAGCTCGGCGATCAGGCCGAAGCCCTGGAAGAGGCGCCGAAGATGGCCAGCAGCACCAGGCAGGCCGGGCCGAAG
       < I V G A R L E A I L G F G Q F L G G F I A L L V L L G P V F
54945 ATCTTGTACGCCTCGGCCTGGGTCGGCGCGTTCAGCGCGGGCTTGAGCAGCGGGGCGAAGAGGAGCAGGTACATCACCGGCTGGAAGACGCC
       < I K Y A E A Q T P A N L A P K L L P A F L L L Y M V P Q F V G
55037 GACGAAGACCGGATTGCGGACGCAGGAGTTGCATCTGGCCGTGGGCGACGAGCCAGGTGTCGCGGGCGAACTTCATGATCGGACT
       < V F V W V P N R L L L Q M Q R Q A V L W T D R A F K M
55127 CCGGGTGGTCAGGACTCGCGCAGCGAGCGGCCGGTCTTGGTGAGGAAGACGTCGTCGAGGCTGGGGCGGTGCAGCTCGATCGAGCTGAGCC
           < • S E R L S R G T K T L F V D D L S P R H L E I S S L R
55218 TGAGGCCGGACTGGTCGAGCCGGCGCAGGACCTGCGGGATGGCGGTGGCCCCCTCGTCGACGGTCAGGCGCAGGCCGCCGCCGTCGACGGTT
       < L G S Q D L R R L V Q P I A T A G E D V T L R L G G G D V T
55310 TCCAGCTTGGTGACGTACGGCTCGGTGTCGAGCAGTTGGGCGGCGTGCGGGGTGGCGGCGTCCAGCCCGAGCAGCACCTCGCCGGA
       <E L K T V Y P E T D L L Q A A Q P T A A A D L G V L L V E G S
55402 GATCTCCCGCTTCAGCCCGCCCGGCGTACCCTCGGCGACCACCTCGCCGTGGTCCATGATCGCGATCCGGTCGCAGAGCGCGTCGGCCTCGT
       < I E R K L G G P T G E A V V E G H D M I A I R D C L A D A E D
55494 CCAGGTAGTGCGTGGTGATGAAGACGGTCATCCCCCTCGGCGCGCAGCCGACGGATCTCGTCCCACATGTGGGCGCGACTCTGCGGGTCGAGG
       < L Y H T T I F V T M G E A R L R R I E D W M H A R S Q P D L
55586 CCGCTGGTCGGCTCGTCCAGGAAGACAATGCGGGGGCGTGGATGATGCGGAGAGCGATCTCGACGGCCGGGAGTAGGT
       <G S T P E D L F V I R P D H I I G L A I E V R R R Q G G S Y T
55678 CTTGCACTTACGGTCGGCGTACTCGGTGAGCTGGAAGGCGGCCAGTGCGCGCTCGGCGCGGCGGAGGGCGTCGGCCTTGCCGATGCCGTACA
       < K C K R D A Y E T L Q F A A L A R E A R R L A D A K G I G Y M
55770 TCCGGGCGTCGCAGGACCAGTTCCTCGCGGGCGGTGGAGTCGTCCCAGGTGCTGCCGCCCTGGGCGACATAGCCGATCCGGCGACGCACCTCG
       < R A H L E E R A T S D D W T S G G Q A V Y G I R R R V E
55862 GCCCGGGTTCCGCAGCAGGTCGGCCCCGGCGATGGTGGCCTGGCCCGTCGGGGGTGATGAGGGTGGCCAGCATCCGCAGGGTGGTGGTCTT
       <A P N R L L D A G A I T A Q G G D P T I L T A L M R L T T T K
55954 CCCGGCGCCGTTGGGGCCGAGGAACCCGAAGATCTCCCCCTCGGCGACGTCCAGGTCGACGCCGCGCACGGCGTCGACCGTCTTGTGCTGTC
       < G A G N P G L F G F I E G E A V D L D V G R V A D V T K H Q R
56046 GACCGGCCGGGAGCGAAACGACTTCCGCAGCCCTCTGGTCTGGATCATCTTCGCTCCTGGTCGTCCTTAGCCGGACCGGGCCGGCCCTC
       < G A R S R F S K R L G R T Q I M
56136 TCTCCGGGACGCCACGCCACACGGGTGGCCCCGAACGTCGCGCCGAGGCTAACGCGATATAACTTCTCTAGTCAACTTTGATTAATGGCGA
                                                         < • R S I V E R T L K S • H R
56227 CCGTCGGCCCCCTCCCCCACGTTCCAGCCGTCCTGACTGGCCAACCCTTCGGGCAGATACGGCACGCCGGCCTCGATCCGGTCGGCGACCCG
       <G D A G E G V N W G D Q S A L G E P L Y P V G A E I R D A V R
56319 CTCACACCAGGCCACCTCGACCTCTCCCCCGGGCAATCCACAGCTCGTACATCCAGCTCACGCCGACCGGCTTGGAGTCGCGGATCCAGGAGG
       < E C W A V E V E G R A I W L E Y M W S V G V P K S D R I W S S
```

Figure 110

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56411 ACTCCATCGAGGCACGCATGGTTTCGACACTGGCCCGCAGCACCTGCCCCCGACTGCGCAGCGCGGCCACCGCCTCCGGCCTGGGCAGCGCC
      <  E  M  S  A  R  M  T  E  V  S  A  R  L  V  Q  G  R  S  R  L  A  A  V  A  E  P  R  P  L  A
56503 GGCAGGAACGCGAACGCCGCCACGAACGGATCGCTCGTCTGATGATTGCCCCACCACAGGCCGCGCAGCAGCGTCTCGAACTCGTCGACCCC
      <  P  L  F  A  F  A  A  V  F  P  D  S  T  Q  H  N  G  W  W  L  G  R  L  L  T  E  F  E  D  V  G
56595 CTTCGGGGTGATCTCGTACGTCGTCCGCGCCCGCCGGGCGCCGACCTGCTCGGTGGCGACCTCGCGGAGCAGCCCCTCCTCGCCGAGCTTGC
      <  K  P  T  I  E  Y  T  T  R  A  R  R  A  G  V  Q  E  T  A  V  E  R  L  L  G  E  E  G  L  K  R
56687 GCAGCGCGTGGTAGATCGAGCCGGGCTGCACGTTGGCCCACTTGTCGGCACCCCAACTGAGCAGCTCGCGGCGGACGTCGTAGCCGTGCACC
      <  L  A  H  Y  I  S  G  P  Q  V  N  A  W  K  D  A  G  W  S  L  L  E  R  R  V  D  Y  G  H  V
56779 GGCTGCATCCACTTGACCAGGCCGAGAATCATCATGCGAGTGGCAGACACCGGAAAAGCGTATTAGACAAGTTTGACTATCCAAGCATCTG
      <  P  Q  M  W  K  V  L  G  L  I  M  M
56870 GGCAGTGCCTCATCCCACACTGAGCGATCGTTAGGGCCACGACGCCGGCCGATAAACTCCCCGTCAGTAACATCCCGGGAGGAGCCACGAG
56961 GTGCGCAAGGTACTCATCGCCAACCGAGGCGAGATCGCCGTCCGCGTCATCCGCGCCTGCCGCGACGCCGGCCTGGGCAGCGTCGCCGTCT
      >  V  R  K  V  L  I  A  N  R  G  E  I  A  V  R  V  I  R  A  C  R  D  A  G  L  G  S  V  A  V
57052 ACGCGGACTCCGACCGGGACGCCCTGCACGCGACCCTGGCCGACGAGGCGTACGCCCTGGGCGGCGACACCGCCGCCGAGACGTACCTGCGG
      >  Y  A  D  S  D  R  D  A  L  H  A  T  L  A  D  E  A  Y  A  L  G  G  D  T  A  A  E  T  Y  L  R
57144 ATCGACAAGCTGATCGCCGTCGCGGGCACAGGCCGGGGCCGACGCCGTCCACCCCGGGTACGGCTTCCTCGCCGAGAACGCCGACTTCGCCCA
      >  I  D  K  L  I  A  V  A  A  Q  A  G  A  D  A  V  H  P  G  Y  G  F  L  A  E  N  A  D  F  A  Q
57236 GGCCGTCCTCGACGCCGGGCTTACCTGGATCGGCCCGACCCCACAGGCGATCCGCGACCTGGGCGACAAGGTCACCGCCCGGCACATCGCCC
      >  A  V  L  D  A  G  L  T  W  I  G  P  T  P  Q  A  I  R  D  L  G  D  K  V  T  A  R  H  I  A
57328 AGCGGGCCGGCGCGCCCCTGGTTCCCGGTACCTCGGACCCGGTCGGCAGCCCGGACGAGGTGATCGCATTCGCGGTCGACCACGGCCTGCCG
      >  Q  R  A  G  A  P  L  V  P  G  T  S  D  P  V  G  S  P  D  E  V  I  A  F  A  V  D  H  G  L  P
57420 GTCGCGCCATCAAGGCCGCCTTCGGCGGCGGCGGGCGGCTCAAGGTGGCCCGCACGATGGAGGAGATCCCGCACCTGTTCGAGTCGGCCAC
      >  V  A  I  K  A  A  F  G  G  G  G  R  G  L  K  V  A  R  T  M  E  E  I  P  H  L  F  E  S  A  T
57512 CCGGGAGGCGGTCGCGGCGTTCGGCCGGGGCGAGTGTTTCGTCGAGCGGTACCTCGACCAGCCCCGGCACGTCGAGGCCCAGGTCCTCGCCG
      >  R  E  A  V  A  A  F  G  R  G  E  C  F  V  E  R  Y  L  D  Q  P  R  H  V  E  A  Q  V  L  A
57604 ACCAGCACGGCAACGTGATCGTCGTCGGCACCCGGGACTGCTCGCTGCAACGCCGGCACCAGAAACTCGTCGAGGAGGCCCCCGCGCCGTTC
      >  D  Q  H  G  N  V  I  V  V  G  T  R  D  C  S  L  Q  R  R  H  Q  K  L  V  E  E  A  P  A  P  F
57696 CTCACCGACGCCCAGCGCCGGCAGATCCACGACAGCGCCAAGGCAATCTGCCGGGGAGGCCGGCTACCACGGCGCCGGCACCGTGGAGTACCT
      >  L  T  D  A  Q  R  R  Q  I  H  D  S  A  K  A  I  C  R  E  A  G  Y  H  G  A  G  T  V  E  Y  L
57788 GGTGGGCACGGACGGCACGATCTCCTTCCTTGAGGTCAACACCCGCCTGCAGGTCGAGCACCCGGTCACCGAGGAAACCGCCGGCATCGACC
      >  V  G  T  D  G  T  I  S  F  L  E  V  N  T  R  L  Q  V  E  H  P  V  T  E  E  T  A  G  I  D
57880 TCGTCCGCGAGCAGTTCCGGATCGCCGACGGCGAGAAGCTGCGGCTGGCCGAGGATCCGACCCCGCGCGGGCACTCCATCGAGTTCCGGATC
      >  L  V  R  E  Q  F  R  I  A  D  G  E  K  L  R  L  A  E  D  P  T  P  R  G  H  S  I  E  F  R  I
57972 AACGGCGAGGATCCGGGCCGCAACTTCCTGCCCGCCCCGGCACCGTCACCGCGCTGCGGCTGCCCACCGGCCCCGGTGTCCGGGTGGACAC
      >  N  G  E  D  P  G  R  N  F  L  P  A  P  G  T  V  T  A  L  R  L  P  T  G  P  G  V  R  V  D  T
58064 CGGCATCTCCGCCGGCGACGTGATCGGCGGCAACTTCGACTCCCTGCTGGCCAAGGTGATCATCACGGGCGAGACCCGCACCGAGGCCCTGG
      >  G  I  S  A  G  D  V  I  G  G  N  F  D  S  L  L  A  K  V  I  I  T  G  E  T  R  T  E  A  L
58156 AGCGGGCCCGGCGCCTGGACGAGATGGTCGTCGAGGGAATGGCCACGGCGCTGCCGTTCCACCGCCTGGTGGTACGCGACCCCGCGTTC
      >  E  R  A  R  R  A  L  D  E  M  V  V  E  G  M  A  T  A  L  P  F  H  R  L  V  V  R  D  P  A  F
58248 ACCGCCGCGCCGTTCACCGTGCACACCCGGTGGATCGAGACGGAGTTCGACAACACCGTCCTGCCGTTCACCGCCGCCGGCCCCGCCGA
      >  T  A  A  P  F  T  V  H  T  R  W  I  E  T  E  F  D  N  T  V  L  P  F  T  A  A  A  G  P  A  E
58340 GGGCCCGGCCGAGCGGGAGACCGTCGTGGTCGAGGTGGGCGGCAAGCGGCTGGAGGTGACCCTCCCCGCCGGCCTCGGCGCGGGTACGGCCG
      >  G  P  A  E  R  E  T  V  V  V  E  V  G  G  K  R  L  E  V  T  L  P  A  G  L  G  A  G  T  A
58432 CCGGGCCCGGCCGAGCGGGAAGCCGGCCCGGCGGGGCGGCGGGGCCGGCGCGGCGGCGGGCTCGGCGGCGACGCCCTCACCTCTCCGATGCAG
      >  A  G  P  A  A  R  K  P  A  R  R  G  G  G  A  K  A  G  A  A  V  G  G  D  A  L  T  S  P  M  Q
58524 GGCACGATCGTGAAGATCGCCGTCGCGGACGGGGACACCGTCGCCAAGGGCGACCTGGTCGTCGTGCTGGAGGCGATGAAGATGGAGCAGCC
      >  G  T  I  V  K  I  A  V  A  D  G  D  T  V  A  K  G  D  L  V  V  V  L  E  A  M  K  M  E  Q  P
58616 GCTGCACGCGCACAAGGCGGGCACGGTCGGCGGGCTGTCCGCCGAGGTCGGCGCGGTCCTCGCCGCCGGCGCCCCCATCTGCACCATCACCT
      >  L  H  A  H  K  A  G  T  V  G  G  L  S  A  E  V  G  A  V  L  A  A  G  A  P  I  C  T  I  T
58708 GAGGTGCAAGGAGGGGCCCCCTGTTAACGCATTCGGTATAGGAAGGGCCCCTTCCTAACCACGCGCCCGGCGGGGCCGCGCCCCAGCCCGGG
      >  •
58800 TACGCGTACCGGCCGGGGGTGTTTTCCGCGACCACCGCGAGCGGTGAGGACCGGGGCCGGGAATGATGGCCAGGTGCGGTTCCTACATGGC
                                                                                 >  >  V  R  F  L  H  G
58891 GCGGTTCCCGCGCACGACCTGACCTACAACGACGTCTTCATGGCGCCGAACCGCTCCGAGGTCGGCTCCCGGTTGGACGTCGACCTGGCCAC
      >  A  V  P  A  H  D  L  T  Y  N  D  V  F  M  A  P  N  R  S  E  V  G  S  R  L  D  V  D  L  A  T
58983 CTCCGACGGCACGGGCACCACCATCCCGCTGGTGGTGGCGAACATGACGGCCGGTGGCCGGCGGATGGCCGAGACTGTCGCCCGGCGGG
      >  S  D  G  T  G  T  T  I  P  L  V  V  A  N  M  T  A  V  A  G  R  R  M  A  E  T  V  A  R  R
59075 GCGCACTCGCGGTGATCCCGCAGGACATCCCGATCGAGGTGGTGGCCAACGTGGTCGCCTGGGTCAAGCAACGGCACCTGGTGCACGACACG
      >  G  A  L  A  V  I  P  Q  D  I  P  I  E  V  V  A  N  V  V  A  W  V  K  Q  R  H  L  V  H  D  T
59167 GCGATCACGCTCGGGCCCCACCGACACCGTCGGCGATGCCATCCATCTGCTGCCGAAACGGTCGCATGGCGCGGTGGTGGTGGTCGACGAGGC
      >  A  I  T  L  G  P  T  D  T  V  G  D  A  I  H  L  L  P  K  R  S  H  G  A  V  V  V  D  E  A
59259 CGGTCGGCCGCTGGGCGTGGTGACGGAGGCGGACACCGTCGGGGTGGACCGCTTCGCCCAGCTCCGCCACGTGATGTCGACCGAGTTGCACA
      >  G  R  P  L  G  V  V  T  E  A  D  T  V  G  V  D  R  F  A  Q  L  R  H  V  M  S  T  E  L  H
59351 CGGTGCCGGCGGACGCGGACCCGCGTACCGGATTCGACCGGCTCTCGGCGGGCCGGCGGCGGCTCGCGCCGGTGGTGGACGGCGACGGCCGG
      >  T  V  P  A  D  A  D  P  R  T  G  F  D  R  L  S  A  G  R  R  R  L  A  P  V  V  D  G  D  G  R
59443 CTCGTCGGGGTGTTGACCCGCAAGGGCGCGCTGCGCGCGGACCCTCTACACCCCGGCGGTGGACGACCGGGGCCGGCTGCGGATCGCGGCGGC
      >  L  V  G  V  L  T  R  K  G  A  L  R  A  T  L  Y  T  P  A  V  D  D  R  G  R  L  R  I  A  A  A
59535 CGTCGGCATCAACGGCGACGTCACCGGCAAGGCCGCCGCGCTGCTGGAGGCCGGGGTCGACGCCCTGGTGGTGGACACCGCGCACGGCCACC
      >  V  G  I  N  G  D  V  T  G  K  A  A  L  L  E  A  G  V  D  A  L  V  V  D  T  A  H  G  H
59627 AGGCGCGGATGGTCGCCGCGCTGCGGGCGGTGCGCAAGCTTCACCCGGGCGTTCCGGTCGCGGCCGGCAACGTGGTCACCGCCGATGGGGTA
      >  Q  A  R  M  V  A  A  L  R  A  V  R  K  L  H  P  G  V  P  V  A  A  G  N  V  V  T  A  D  G  V
59719 CGCGACCTCGTCGAGGCCGGCGCCGACATCGTGAAGGTGGGCGTCGGTCCGGGCGGCGATGTGCACCACCCGGATGATGACCGGGGTGGGGCG
      >  R  D  L  V  E  A  G  A  D  I  V  K  V  G  V  G  P  G  A  M  C  T  T  R  M  M  T  G  V  G  R
59811 TCCGCAGTTCTCCGCGGTGCTGGACTGCGCGGCGGCGGCGCGGGACCTCGGCCGGCACGTCTGGGCCGACGGCGGGGTACGGCACCCGCGCG
      >  P  Q  F  S  A  V  L  D  C  A  A  A  A  R  D  L  G  R  H  V  W  A  D  G  G  V  R  H  P  R
59903 ACGTGGCGGTGCTGGCCCTCGCCGGCGCGTCGAACGTGATGATCGGTTCCTGGTTCGCCGGCACGTACGAGTCCCCGGGTGACCTGTACACG
      >  D  V  A  L  A  L  A  A  G  A  S  N  V  M  I  G  S  W  F  A  G  T  Y  E  S  P  G  D  L  Y  T
59995 GACGCGGACGGCCGGAGGTACAAGGAGAGCTTCGGGATGGCCTCGTCGCGGGCGGTCAGCGCGCGTACGCCGAGGACAGCGCGTTCGACCG
      >  D  A  D  G  R  R  Y  K  E  S  F  G  M  A  S  S  R  A  V  S  A  R  T  A  E  D  S  A  F  D  R
```

Figure 11P

```
60087 GGCCCGCAAGGGGATCTTCGAGGAGGGCATCTCCTCGGCCCGGATGTACCTCGACCCGGATCGCCCGGGCGTCGAGGACCTGATCGACGAGA
      >  A  R  K  G  I  F  E  E  G  I  S  S  A  R  M  Y  L  D  P  D  R  P  G  V  E  D  L  I  D  E
60179 TCATCTCCGGGGTACGCAGCGCGTGCACGTACGCGGGCGCGCGCAGCCTGGCGGAGTTCGCGGAGCGGGCGCTGGTCGGGGTGCAGAGCACG
      >I  I  S  G  V  R  S  A  C  T  Y  A  G  A  R  S  L  A  E  F  A  E  R  A  L  V  G  V  Q  S  T
60271 GCCGGCTACACCGAGGGGATGCCCCTACCGACGAGTTGGTGACCCCGCGCCCGGCGGTGAGAAGGGTTCCCCTCTCTACCGGAGGCGTCAA
      >  A  G  Y  T  E  G  M  P  L  P  T  S  W  ●
60362 CAAGGGGCCCTTCCTTCGTGCGCGGCTGGGTATCGGCGTGACCGACTGCCGCACGCGCCGCCGCACACTGAGCCGCCGCCCGTCGAGGGCCC
60454 ACCGAACGGGCGCCGGGGTCAGTCGAAGAGGCGACGGATGACGGTCCGGGCGGCGGCCTCCGGGTCCGGGCCGGTGCCGGGCGGGAGCGCC
                  <  ●  D  F  L  R  R  I  V  T  R  A  A  A  E  P  D  P  G  T  G  P  P  L  A
60545 CCGGCCAGCCAGAGTGTCACGAAGCCGTGCACGATCGACCAGCGGCCAGGGCGTCCGCCTCCTGGTCCGGGTCGGTTTCCCGGCGCGGGAG
      <G  A  L  W  L  T  V  F  G  H  V  I  S  W  A  A  L  A  D  A  E  Q  D  P  D  T  E  R  R  P  L
60637 GGCGGCCCACCCGGCCCGGCAGCGCCGCGCCGGCCCGATCACGGGCGGCTGTCACCTCGGGGTCGTCGCGACGGTAGAGCTCCGGGCGGAACA
      <  A  A  V  G  A  R  L  A  A  G  A  R  D  R  A  A  T  V  E  P  D  D  R  R  Y  L  E  P  R  F  M
60729 TCACCTCGAAGTGGGCCCGGTGGTCGACCGCGAACCGGACGTACGCCACGCCGGCGTCGAGCAGGTCGCCGGCCTCGCACAGCGCCCCGGCC
      <  V  E  F  H  A  R  H  D  V  A  F  R  V  Y  A  V  G  A  D  L  L  D  G  A  E  C  L  A  G  A
60821 AGCAGGTCGAATCCCTCGACGGCGAGCGCGGTGAGCAGCCCCGCCTTGTCGCCGAAGTGGTGCGCGGGGGCGGCGTGCGAGACCCCGGCCCG
      <L  L  D  F  G  E  V  A  L  A  T  L  L  G  A  K  D  G  F  H  H  A  P  A  A  H  S  V  G  A  R
60913 GCGGGGCCAGGTCGCGCAGGCTCAGGGCGGCCGGCCCGGCGTCGGTGATCGCGTCGACGGCGGCGGCGAGCAGGGCGGCGACGCAGGTCACCGT
      <  R  A  L  D  R  L  S  L  A  A  P  G  A  D  T  I  A  D  V  A  A  A  L  L  A  R  R  L  D  G  H
61005 GATGGTAGCCACGCGGTCCGGTCATGCCGGCAGCCTAACTTGTCATTGACAAGATAGCCAGGCCGAAGCAATCTAGGCAATGACAAGTTG
      <  H  Y  G  R  P  G  T  M
61095 CCTTCGACCGAGGAGAACCCCGATGGCGCCCCTGATCGCTCTCATCGCCGGCTCGGCCCTGGCCCGACTCGCCGGGCTACTCAACGTCGACG
61187 CCCTGGCCGGCTGGCACCCCGCCCTGCGGGTCGGGCTCGCGGCCATGTTCGCGCTCACCGGGATCGCCCACTTCACCTCCCGACGGCCCGAC
61279 CTGGTCGCCCATGGTGCCGCCCTGCGCCCACCCGGGGCTGCTGGTGACGGTCACCGGGCTGCTGGAGTTGGCCGGCGCGGTCGCGCTGCT
      >  M  V  P  P  R  L  P  H  P  G  L  L  V  T  V  T  G  L  L  E  L  A  G  A  V  A  L  L
61371 CGTCCCCCGGCACGGCGCGGTGGGCAGCGGCCGGGCTGGGCTGCTGCTGCTCGCGATGTTCCCGGCCAACGCCTCGGCCGCCCGGCGCGGGC
      >  V  P  G  T  A  R  W  A  A  A  G  L  G  L  L  L  L  A  M  F  P  A  N  A  S  A  A  R  R  G
61463 TGACCCTGGCCGGCCGGCCGGTGACCCCGCTCGTCCCCCGCGCGCTGCTCCAGGTGATCTTCCTCACCGCCGCCGCCGCGATTTCGTTTGGG
      >L  T  L  A  G  R  P  V  T  P  L  V  P  R  A  L  L  Q  V  I  F  L  T  A  A  A  A  I  S  F  G
61555 CCCTGACTATCAGGGAGCTAACATGACCCGCATGGAGCTGATAGGGCTGCGAGACGTGCCACTCGGCCGGCTGCTGGTGACCGCCGGCCA
      >  P  ●                                              >  V  P  L  G  R  L  L  V  T  A  G  H
61645 CGTCGTCGGCCAACGGTGGAACCGCTACCTCGCCGAGGAGCACGGCCTCACCCAGGCGGGCATGGTCACCCTGATGACCCTGGCCCGGCACG
      >  V  V  G  Q  R  W  N  R  Y  L  A  E  E  H  G  L  T  Q  A  G  M  V  T  L  M  T  L  A  R  H
61737 GCGAGCTGCCGCACCGGGCGGTCGCCGAGGCGTGCTTCATCCGCCCGGCCACCCTAACCGGCATCGTCGACACACTGGAGCGCGACGGCCTC
      >G  E  L  P  H  R  A  V  A  E  A  C  F  I  R  P  A  T  L  T  G  I  V  D  T  L  E  R  D  G  L
61829 GTCGAGCGGCAACGCGACGACGTCGACCGGCGCAGCGTGCGGCTCGTCCTGACCCCCGCCGGTCGGGAACGGGTCGCCGCGCTCACCAACGT
      >  V  E  R  Q  R  D  D  V  D  R  R  S  V  R  L  V  L  T  P  A  G  R  E  R  V  A  A  L  T  N  V
61921 CATGCAGTCCGGACGACCGATGACCTCGGTCGACGCCGACCCGGCGAAGGCCGCCGTGATCCGGCAGTTCCTGCTCGAGGTCATCGGCAGTG
      >  M  Q  S  G  R  P  M  T  S  V  D  A  D  P  A  K  A  A  V  I  R  Q  F  L  L  E  V  I  G  S
62013 GAGAGGAACCTCGGGTGACGGCCCTCGACGCGAGGCCGGAGGCTCCGGCATGCTGATCCGGCTGCTCCGCGCCCACCTGCGCCCGTACCGTC
      >G  E  E  P  R  V  T  A  L  D  A  R  P  E  A  P  A  C  ●
62105 GACCGCTGGCGGCGGTGATGGCGTTGCAGTTCGTCGGCACGATGGCCTCGCTCTACCTGCCGAGCCTCAACGCCGACATCATCGACCAGGG
                  >  M  A  L  Q  F  V  G  T  M  A  S  L  Y  L  P  S  L  N  A  D  I  I  D  Q  G
62196 TGTGGCCCGGGGCGACACCGGTACATCATGCGTACGGGCGGCTGGATGCTGCTGGTCAGCCTGGTGCAGATCGCCTGCTCCACCGCCGCGG
      >  V  A  R  G  D  T  G  Y  I  M  R  T  G  G  W  M  L  L  V  S  L  V  Q  I  A  C  S  T  A  A
62288 TCTTCCTCGGCGCGCGCTCCGCGATGGGCTTCGGCCGGGACGTACGCGCCGAGGTCTTCGCCCACGTCAACCGGTTCTCCGCCCGCGAGGTG
      >V  F  L  G  A  R  S  A  M  G  F  G  R  D  V  R  A  E  V  F  A  H  V  N  R  F  S  A  R  E  V
62380 ACCCGCTTCGGCGCACCCTCGCTGATCACCCGCAACACCAACGACGTGCAACAGGTGCAGATGCTCGTCCTGATGAGCTGCACCATGCTGGT
      >  T  R  F  G  A  P  S  L  I  T  R  N  T  N  D  V  Q  Q  V  Q  M  L  V  L  M  S  C  T  M  L  V
62472 CGCCGCCGATCATGAGCGTCGGCGGGGTGTTCATGGCACTGCGGGAGGACGTCGGGCTGTCCTGGCTGATGCTGGTCAGCGTGCCGGCCGC
      >  A  A  P  I  M  S  V  G  G  V  F  M  A  L  R  E  D  V  G  L  S  W  L  M  L  V  S  V  P  A
62564 TGGCGATCGCCCTGATGCTGATCATCCGGCGGATGGTGCCCGGGTTCCGGCTGATGCAGACCCGCATCGACGCGGTCAACCGCGTGCTGCGC
      >L  A  I  A  L  M  L  I  I  R  R  M  V  P  G  F  R  L  M  Q  T  R  I  D  A  V  N  R  V  L  R
62656 GAGCAGATCACCGGCATCCGGGTGGTCCGGGCGTTCGTCCGCGAGCCGTACGAGACGGCGCGCTTCGGCCGCGCGAACGCCGACCTCACCGC
      >  E  Q  I  T  G  I  R  V  V  R  A  F  V  R  E  P  Y  E  T  A  R  F  G  R  A  N  A  D  L  T  A
62748 GACCGCCCTGCGCACCGGTCGGTTGATGGCCCTGATCTTCCCCGTGGTGACGCTGGTGCTCAACGTCTCCAGCGTCGCCGTGCTGTGGTTCG
      >  T  A  L  R  T  G  R  L  M  A  L  I  F  P  V  V  T  L  V  L  N  V  S  S  V  A  V  L  W  F
62840 GCGCCGGACCGCGTCGACGCCGGCCAGATCCAGGTCGGCGCGCTCACCGCCTTCCTGCAGTACCTCATGCAGATCCTGATGGCCGTCATGTTG
      >G  A  D  R  V  D  A  G  Q  I  Q  V  G  A  L  T  A  F  L  Q  Y  L  M  Q  I  L  M  A  V  M  L
62932 GCCACCTTCATCCTGATGATGGTCCCCGCGCCGCCGGTCTGCGCCGAGCGGATCGTCGAGGTGCTCGACACCGACTCGACGGTGATCCCGCC
      >  A  T  F  I  L  M  M  V  P  R  A  A  V  C  A  E  R  I  V  E  V  L  D  T  D  S  T  V  I  P  P
63024 GGCCGCGCCGACGCCGAGGTGACCGGCCGGGGCGAACTGGAACTGCGCGGCGTCCGGTTCCAGTACCCGGGGGCGAGCGCCGGTGCTGC
      >  A  A  P  T  A  E  V  T  G  R  G  E  L  E  L  R  G  V  R  F  Q  Y  P  G  A  S  A  P  V  L
63116 ACGACATCTCGTTCCGGGCCACGCCCGGGCGCACCACGGCCATCATCGGCAGCACGGGGGCCGGCAAGACGACCCTGCTGACGCTGATCCCC
      >H  D  I  S  F  R  A  T  P  G  R  T  T  A  I  I  G  S  T  G  A  G  K  T  T  L  L  T  L  I  P
63208 CGGCTGATCGACGCCACCGCCGGGGCGGTGCTGGTCGACGGGGTGGACGTGCGTGACCTGGCCCCGGACGATTTGTGGCGGCGGATCGGGCT
      >  R  L  I  D  A  T  A  G  A  V  L  V  D  G  V  D  V  R  D  L  A  P  D  D  L  W  R  R  I  G  L
63300 GGTGCCGCAGCGGCCGTACCTGTTCAGCGGCACGATCGCCAGCAACCTGCGGTACGGCAACCCGGACGCCACCGACGCGGAGCTGTGGGCCG
      >  V  P  Q  R  P  Y  L  F  S  G  T  I  A  S  N  L  R  Y  G  N  P  D  A  T  D  A  E  L  W  A
63392 CCCTGGAGATCGCCCAGGCGCGCGACTTCGTCGCCGAGTTGCCCGAAGGGCTGAACGCCCCGATCACGCAGGGCGGCACCAATATCTCCGGC
      >A  L  E  I  A  Q  A  R  D  F  V  A  E  L  P  E  G  L  N  A  P  I  T  Q  G  G  T  N  I  S  G
63484 GGGCAGCGCCAGCGCCTCGCGATCGCCCGGGCCCTGGTCCGCAAGCCGGAGATCTACCTGTTCGACGACTCGTTCTCGGCGCTCGACCTGG
      >  G  Q  R  Q  R  L  A  I  A  R  A  L  V  R  K  P  E  I  Y  L  F  D  D  S  F  S  A  L  D  L  G
63576 CACCGACGCCCGGCTGCGCGCGGCGCTACGACCGGTCACCGCGGACGCGACGGTGCTGATCGTGGCCCAGCGGGTCTCCACGATCGTCGACG
      >  T  D  A  R  L  R  A  A  L  R  P  V  T  A  D  A  T  V  L  I  V  A  Q  R  V  S  T  I  V  D
63668 CCGACCAGATCATCGTGCTTGAGGACGGGGGCATCGTCGGGATGGGCCGACACGCCGAACTACTGGAAGACTGCCCCGACGTACGCGGAGATC
      >A  D  Q  I  I  V  L  E  D  G  G  I  V  G  M  G  R  H  A  E  L  L  E  D  C  P  T  Y  A  E  I
63760 GTCGCTCCCAGCAGAGCGGCGGGGGTGCCGGCCATGCAGCGGCGTACCGGATCAGCGGCCCACCGCGCGGCCGGCGGAGGGGCCGACGCCGAA
      >  V  A  S  Q  Q  T  A  G  V  P  A  ●
```

Figure 11Q

```
63851 GCGGCTGCCCTCCGGCAACCAGGGCAGCGGCCCGAGGTGGATGAGCGCCGGCATGCCGGCCGAGAAGTCGATGAACTTCGGGCCGTCCAC
                                    > M  S  A  G  M  P  A  E  K  S  M  N  F  G  P  S  T
63941 CCGCCGGCTGCTGCGCCGGCTGCGACCGCACCGCCTCCAGCTGGCCGCCATCGTCCTGCTCTCGCTGGTCAGCGTCGGTTGCAACGTGTACG
       > R  R  L  L  R  R  L  R  P  H  R  L  Q  L  A  A  I  V  L  L  S  L  V  S  V  G  C  N  V  Y
64033 GGCCGAAGGTGCTCGGCCACGCCACCGACCTGATCTTCAGCGGGGTGATCGGCCGGCAGTTGCCGGCCGGCACCACCGCCGAGCAGGCGGTC
      >G  P  K  V  L  G  H  A  T  D  L  I  F  S  G  V  I  G  R  Q  L  P  A  G  T  T  A  E  Q  A  V
64125 GCGGCGGCCCGCGGCGGCTAACGACAGCTTCGCCGACATGCTGGCCCGGATGGACGTGGTGCCCGGGGTGGGCATCGACTTCACCGCCCT
       > A  A  A  R  A  A  G  N  D  S  F  A  D  M  L  A  R  M  D  V  V  P  G  V  G  I  D  F  T  A  L
64217 GGGCCGGGTGCTGCTGTTCGTGCTCGCCCTCTACCTGGCGGCCAGCGTGCTGTTGTGGTGGCAGGGCTGGCTGCTCAACGGGGTGGTGCAGC
       > G  R  V  L  L  F  V  L  A  L  Y  L  A  A  S  V  L  L  W  W  Q  G  W  L  L  N  G  V  V  Q
64309 GCACGGTGCTGCGGCTGCGCGCCGACGTGGAGGACAAGCTGAACCGGCTGCCGCTGCCGTACTTCGACCGGCAGCCCCGGGGCGAGTTGCTC
      >R  T  V  L  R  L  R  A  D  V  E  D  K  L  N  R  L  P  L  P  Y  F  D  R  Q  P  R  G  E  L  L
64401 AGCCGGGTCACCAACGACATCGACAACATCTCGCAGAGCCTCCAGCAGACGCTGAGCCAGCTGCTCACCTCGCTGCTCACCGTGGTCGGCGT
       > S  R  V  T  N  D  I  D  N  I  S  Q  S  L  Q  Q  T  L  S  Q  L  L  T  S  L  L  T  V  V  G  V
64493 ACTGGCCATGATGTTCTGGATCTCGCCGCTGTTGGCGCTGGTGTCCCTGGTCGCGGTGCCGATGTCGGTGGTGGTCACCAGCCTGGTCGCGA
       > L  A  M  M  F  W  I  S  P  L  L  A  L  V  S  L  V  A  V  P  M  S  V  V  V  T  S  L  V  A
64585 AGCGGTCACAGCAGCGGTTCATCGCCCAGTGGACGCATACCGGAGAGCTGAACGGCCAGATCGAGGAGGCGTTCACCGGACACGAGCTGGTC
      >K  R  S  Q  Q  R  F  I  A  Q  W  T  H  T  G  E  L  N  G  Q  I  E  E  A  F  T  G  H  E  L  V
64677 AAGGTCTTCGGCCGGCAGCGCGAGGTGGAGGCCGCCTTCACCGCCAAGAACGAGGAGCTGTTCCGGGCCAGCTTCGGCGCCCAGTTCATCTC
       > K  V  F  G  R  Q  R  E  V  E  A  A  F  T  A  K  N  E  E  L  F  R  A  S  F  G  A  Q  F  I  S
64769 CGGGATCATCATGCCGGCGATGATGTTCATCGGGAACCTCAGCTACGTCGCGATCGCCGTGGTCGGCGGGCTGCGGGTGGCGTCGGGGTCGA
       > G  I  I  M  P  A  M  M  F  I  G  N  L  S  Y  V  A  I  A  V  V  G  G  L  R  V  A  S  G  S
64861 TGAGCATCGGCGACGTGCAGGCATTCATCCAGTACTCCCTGCAGTTCACCCAGCCGCTGACCCGGGTCGCCTCGATGGCCAACCTGCTCCAG
      >M  S  I  G  D  V  Q  A  F  I  Q  Y  S  L  Q  F  T  Q  P  L  T  R  V  A  S  M  A  N  L  Q
64953 TCCGGGGTGGCCTCCGCCGAGCGGGTGTTCGCGGTGCTCGACGCCGAGGAGCAGAGCCCGGACCCGGCGGTGCCGGCCCGGGTCGCCGACCA
       > S  G  V  A  S  A  E  R  V  F  A  V  L  D  A  E  E  Q  S  P  D  P  A  V  P  A  R  V  A  D  Q
65045 GCGCGGTCGCGTCGAATTCGACCACGTCTCATTCCGGTACGAGCCGGACAAGCCGCTGATCACCGACCTGTCGCTGGTCGCCGAGCCGGGGC
       > R  G  R  V  E  F  D  H  V  S  F  R  Y  E  P  D  K  P  L  I  T  D  L  S  L  V  A  E  P  G
65137 ACACGGTTGCCATCGTCGGGGCCGATGGCGCCGGCAAGACCACCCTGGTCAACCTGGTGATGCGCTTCTACGAGCTGGACGCCGGGATC
      >H  T  V  A  I  V  G  P  T  G  A  G  K  T  T  L  V  N  L  V  M  R  F  Y  E  L  D  A  G  R  I
65229 ACCCTCGACGGGGTCGACATCACCACGCTGAGCCGCGACGACCTGCGCGGCCGGATCGGCATGGTGCTCCAGGACACCTGGCTCTTCGGTGG
       > T  L  D  G  V  D  I  T  T  L  S  R  D  D  L  R  G  R  I  G  M  V  L  Q  D  T  W  L  F  G  G
65321 CACGATCCGCGACAACATCGCGTACGGCCGGCCGGACGCGAGCGAGGAGGAGATCGTCGCCGCCGCCCGGGCGACGTTCGTGGACCGGTTCG
       > T  I  R  D  N  I  A  Y  G  R  P  D  A  S  E  E  E  I  V  A  A  A  R  A  T  F  V  D  R  F
65413 TGCGTAGCCTCCCCGACGGCTACGACACCGTCATCGACTCCGAGGGCAGCAACGTCAGCGCCGGCGAGAAGCAGCTCATCACCATCGCCCGG
      >V  R  S  L  P  D  G  Y  D  T  V  I  D  S  E  G  S  N  V  S  A  G  E  K  Q  L  I  T  I  A  R
65505 GCGTTCCTGGCCGAGCCGTCGCTGCTGATCCTCGACGAGGCGACCAGTTCGGTGGACACCCGCACGGAGGTGCTGCTCCAACGGGCCATGGC
       > A  F  L  A  E  P  S  L  L  I  L  D  E  A  T  S  S  V  D  T  R  T  E  V  L  L  Q  R  A  M  A
65597 GGCGCTGCGCTCGGACCGGACCAGCTTCGTGATCGCCCACCGTTTGTCCACCATCCGCGACGCGGACCTGATCCTGATGATGGAGCACGGTC
       > A  L  R  S  D  R  T  S  F  V  I  A  H  R  L  S  T  I  R  D  A  D  L  I  L  M  M  E  H  G
65689 GCATCGTCGAGCAGGGCACCCACGAGCAGCTCCTGGCCGCCCGGGGCGCGTACCACCGGCTTTACCAGGCCCAGTTCACCCAGCCGGACCCG
      >R  I  V  E  Q  G  T  H  E  Q  L  L  A  A  R  G  A  Y  H  R  L  Y  Q  A  Q  F  T  Q  P  D  P
65781 GCCGCCGTCGGGGACCCCGAGCCCCAGCCGCCTCGGTCCGGGGCTGACCGTCGTGGCCCGGTACATCCCGCCCAGCTCCCCGACCCGCAG
       > A  A  V  G  D  P  E  P  Q  P  A  S  V  R  G  。
65872 GGGGCAGCTCCCGGGCCCGGGGCCGGAAGACCAGAGCGTGGTGCGGGCAGAGCGCCGGGCGGAGCACGAACTCGTCGTCGGGGCCCAGCCG
65964 CATCGGCGGGAACATGTCGTCGGCGAAGTGGCCGAGGTCGGGGCCTCGATGACGGTGACGTCAGTGCGGCGCGCCGGGGTTCCCGACGTCG
66056 TGGTCCGTACCGCGCTGCGCATGGGGAGACGGTAGGCCGGCCGGGGCGGGCGCGCATCCGAATTCGGGGCCGGCCCGACGCAGCCGAGACG
66148 CATCCGGTTACCGCGAAGGGCGACAGGCCGCCAGTCGCTACAGTCGGCAACCCGGCCGATGCACAGCGCGCCTCGGGGCGGGCCGCCGGCAC
66240 GGGACCTGCCGGCGGCCCATGGCGGCCCGGTCGTCGGCTACGGGGGGTCCGACACTCGAGGCCGCGCCGACTACGGTACGCCGGCCGTCGGC
66332 GATCCGCCGACCGCCTCCACCCGTACGCCGAGGTTGCCGGCCCCAGCGGGTCCCCGGCCCGCGCCGCTGCCCGACCGCCGCGTCGCCGGCCC
66424 GACGACCCGGTTCGTGGCGGGTGCCGGCGAGGTGGAGCCGCCCAGTTACTCCAGCTCGTCGGAGCATGAGCTGGCGGGACGCCTCGGTGATC
                                                   <  。  E  L  E  H  L  M  L  Q  R  A  A  E  T  I
66515 GAGCCCGACAGGCTCGGGTAGATGGTGATGGTCTGGGCCAACTCGTTGACCGTGAGGTTGTTCTCCACCGCCATGGTGATCGGCAGGATCAG
       <S  G  S  L  S  P  Y  I  T  I  T  Q  A  L  E  N  V  T  L  N  N  E  V  A  M  T  I  P  L  I  L
66607 CTCGCTGGCCTTCGGTGCCACCACCACACCGCCGATCACCTGGCCGCTGGCCGGGCGGCAGAACAGCTTCACGAAGCCGTCGGCGAGGTCGT
       < E  S  A  K  P  A  V  V  G  G  I  V  Q  G  S  A  P  R  C  F  L  K  V  F  G  D  A  L  D  D
66699 CCATCTTCGCCCGGGCGTTGCCCGACAGCGGCAGCATCACCTGGCGGCCGGGGTCTTGCCGGCGTCCACCTCGTCCTGGGAGACGCCGACG
       < M  K  A  R  A  N  G  S  L  P  L  M  V  Q  R  A  P  T  K  G  A  D  V  E  D  Q  S  V  G  V
66791 GTGGCCAACTCCGGGTCGGTGAAGACGTTCGCGGCCACCGTACGCAGCCGCAGCGGCCGGACCGCCTCGCCGAGCGCGTGCCACATCGCGAT
       <T  A  L  E  P  D  T  F  V  N  A  A  V  T  R  L  R  L  P  R  V  A  E  G  L  A  H  W  M  A  I
66883 CCGGCCCTGCATGGCGGCGACGCTGGCCAGCGGCAACACCCCGGTGCAGTCGCCGGCAGCGTAGATCCCGGGGACGTTGGTGCGGGACACCC
       < R  G  Q  M  A  A  V  S  A  L  P  L  V  G  C  D  G  A  A  Y  I  G  P  V  N  T  R  S  V  R
66975 GGTCGACGGTGACGTAGCCGCCCCGGGCCAGCTCGACGCCGTACTCGGCGAGGCCGAGGTTGGCGGTGTTGGGGATCGAGCCGACCGCGATG
       < D  V  T  V  Y  G  G  R  A  L  E  V  G  Y  E  A  L  G  L  N  A  T  N  P  I  S  G  V  A  I
67067 AGCGCGTGCGAGCCGTGCACCAGCCGGCCGTCGGCCAGTTCGACCTCCACCCCGTCGGCGATGCGCTGGACCCTCTCGGCGCGGGAGTTGTT
       <L  A  H  S  G  H  V  L  R  G  D  A  L  E  V  E  V  G  D  A  I  R  Q  V  R  E  A  R  S  N  N
67159 GAGGATCGTCATGCCCCGGGGAGCGGAACACGCGCTCGATCGCCATGCGGCGGTCGGCGGTCCTCCGGTGCCACCCGGTCCCGGGACTGGAGA
       < L  I  T  M  G  R  S  R  F  V  R  E  I  A  M  A  A  D  A  D  E  H  P  M  V  R  D  R  S  S  V
67251 CGAGGGTGACCGGGACCCCCATGGCCAGGTACGCGCTGGCGAACTCGGCACCGGTGACGCCGGAACCGACGACGATCAGGTGCTCGGGCAGG
       < L  T  V  P  V  G  M  A  L  Y  A  S  A  F  E  A  G  T  V  G  S  G  V  V  I  L  H  E  P  L
67343 TGCGGCAGGTCGTACACCTGCCGGCAGGTCAGGATGCGCTCGCCGTCCGGCACGGCCGTGGGGAGCTGGCGGGGGGTGGCGCCGGTGGCGAC
      <H  P  L  D  Y  V  Q  R  W  T  L  I  R  E  G  D  P  V  A  T  P  L  Q  R  P  T  A  G  T  A  V
67435 CAGCACGGTCGACGCGTCGATCGAGTGCTTCTCGGAGCCGTCGGCCGGCGTGACGACGACGGTGGTGTGGCCCAGCATGTCCTCGCCGA
       < L  V  T  S  A  D  I  S  H  K  E  S  G  D  A  P  T  V  V  V  R  H  T  H  G  L  M  D  E  G  L
67527 GCCGGGCGTGCCGGCCACGAAGGTGACGCCGGCTTTCACCAGCTTCGCGTGGATGTCGGCGGACTGGGCCAGGGCGAGCCGCTTGACCCGC
       < R  A  T  G  A  V  F  T  V  G  A  K  V  L  K  A  H  I  D  A  S  Q  A  L  A  L  R  K  V  R
67619 TCGTGCACGGCCCGGGCGTCGACGGTGACCGCCTCCAGCCGTCGGAGTGCACCCGAACTCCTCGGTGTCCCGGTACCCGGTGACCACCTC
       <E  H  V  A  R  A  D  V  T  V  A  E  L  G  D  S  H  V  G  F  E  E  T  D  R  Y  G  T  V  V  E
```

Figure 11R

```
67711 CGAGCTGGCCGATGAACGTTTTCGACGGTACGCAGTCGGACAGCACGCAGGCACCGCCGGCCCCCTCGGCCTCCACCACGGTGACATCAGCGT
         <  S  S  A  I  F  T  K  S  P  V  C  D  S  L  V  C  A  G  G  A  G  E  A  E  V  V  T  V  D  A  D
67803 CCAACTGGGCGGCGACCAGGGCCGCCTCGTACCCGGCCGGCCCCCCGCCGATGATCACGATCTGGCTCACAGCTATCGCCCCTCGTCCGT
         <  L  Q  A  A  V  L  A  A  E  Y  G  A  P  G  G  G  I  I  V  I  Q  S  V
67893 GCTCACAGTGACTTTCTTCTCCCCGACGCGTCCGACACGCACCGTCGTATTCTCCCCCAGCCGTCCGCCGGGCTATCGTCATCGCCGTGCG
                                                                                                >  V  R
67984 TCACTACGCCGCCTACGGCTCAAACCTGGACCCCGCCCGGATGCGCGCCTACTGCCCGCACTCCCCGATGGTCGGCGTCGGCTGGCTGGAGG
          >  H  Y  A  A  Y  G  S  N  L  D  P  A  R  M  R  A  Y  C  P  H  S  P  M  V  G  V  G  W  L  E
68076 GCTGGCGGCTCACCTTCGCGGGTGAGGGCGCGATCGGCTGGGAGGGCGCGGTCAGCACCATCGTCGAGTCCCCCGGTGATGGGTGTTCGTG
          >G  W  R  L  T  F  A  G  E  G  A  I  G  W  E  G  A  V  S  T  I  V  E  S  P  G  D  R  V  F  V
68168 GCGCTCTACGACATCCACCCGTACGACGCCGTCCAGCTCGACGAGATCGAGGGGGTGGCCTCCGGGACGTACCGCAAGCTGCACGTCCGCGT
          >  A  L  Y  D  I  H  P  Y  D  A  V  Q  L  D  E  I  E  G  V  A  S  G  T  Y  R  K  L  H  V  R  V
68260 CTCCACCCTCGACGGCGACGTGACCGCGTGGGTCTACGTCTTCGACGGGTACGAGGGCGGCCTGCCGACGGCGTGGTATCTGTCGGAGATCG
          >  S  T  L  D  G  D  V  T  A  W  V  Y  V  F  D  G  Y  E  G  G  L  P  T  A  W  Y  L  S  E  I
68352 CCAACGCCGCCGAGAAGGCGGGCGCGCCCGACGACTACGTCAGCGAGCTGCGGTCCCGCCCCACCGGCACGGCGTCGGCGTAGCGCGTCTC
          >A  N  A  A  E  K  A  G  A  P  D  D  Y  V  S  E  L  R  S  R  P  T  G  T  A  S  A  °
68443 CCACACTCCCAGTCTGCTCCGCCCGAGACGGGGCCGCACGGCGGCCCCCGCCGGGGGTCGTCTGTCACACATCATGGTCGCGCCCGTCACA
                                                                                      <  °  V
68534 CCGCCGTGGCGGCGGGGACGGTGCGCTCGTACATGTCGGTCCAGCGCATCTCGCGCAGCCCCACCGAGCGGTAGAGCGTCGCCGGGGAGGTC
          <  A  T  A  A  P  V  T  R  E  Y  M  D  T  W  R  M  E  R  L  G  V  S  R  Y  L  T  A  P  S  T
68626 GGGTTGGTCAGGTCGACGCCGAGGCCGGCGTGCCGCCGTCCCTTCGCCGCGTAGACCGTGAAGGCCCGCCACAGCAGCGCGGCGCCGACCCC
          <P  N  T  L  D  V  G  L  G  A  H  R  R  G  K  A  A  Y  V  T  F  A  R  W  L  L  A  A  G  V  G
68718 GTGCCGCCGGTACTTCGGCAGCACCGACAGGGTCCGCACCCAGCCCGAGTCCTGTTCCAGCGCCTGGTCGGACGACTGCAACGCCGCCGGCCG
          <  H  R  R  Y  K  P  L  V  S  L  T  R  V  W  G  S  D  Q  E  L  A  Q  D  S  S  Q  L  A  G  P
68810 GCTCCCCGTCGACCTCGGCGACGAACCACTCGTCCCAGGTCCTGTCGTACGCGGGCAGACGCTCCCGCCAGTGGTCGTACCCGGCCGGCTCG
          <  E  G  D  V  E  A  V  F  W  E  D  W  T  R  D  Y  A  P  L  R  E  R  W  H  D  Y  G  A  P  E
68902 TAGTCCGGGGTGTCCCGGAACGCCGTGTCGTAGATCCGGTGGAACAGGCGCAGGTCGTCCTCGTCGCCGGCGCGCAGCGGCCGGACCGTCAC
          <Y  D  P  T  D  R  F  A  T  D  Y  I  R  H  F  L  R  L  D  D  E  D  G  A  R  L  P  R  V  T  V
68994 CCCGGGTGGGGCGGCGGCTCGGCGGGCAGCCCGGCCAGGTCACGACTCATCCGTACGTACCGCTTCACCCGGCTGAAACCGGCCTCGGTCA
          <  G  P  P  P  P  E  A  P  L  G  A  L  D  R  S  M  R  V  Y  R  K  V  R  S  F  G  A  E  T  L
69086 GCTCCGTCACCCAGCGGGTCTCCGGCGGGTAGGCCGAGGCGCGGACGGTCAGCGCGGGCAGGCTCCGCTCCGCGGCCCGCTCGGCGACCCGG
          <  E  T  V  W  R  T  E  P  P  Y  A  S  A  R  V  T  L  A  P  L  S  R  E  A  A  R  E  A  V  R
69178 TCCAGCATCAGAGCGAGCAGCGGGGCGCGTACCGCCTCGGCGCGCTCCGGGTCGACGAGGACGTCGACGAACTCCCGGCCCACCCCGGTCGG
          <D  L  M  L  A  L  L  P  A  R  V  A  E  A  R  E  P  D  V  L  V  D  V  F  E  R  G  V  G  T  P
69270 GTTGTCCACCACCGACCAGGCGACGAGCCGGCCCTGCGGGTCGCTGACCAGCCAGGAGTCGCGCGCCGGGTCGAAGAAGGGGGCCGTCAGGG
          <  N  D  V  V  S  W  A  V  L  R  G  Q  P  D  S  V  L  W  S  D  R  A  P  D  F  F  P  A  T  L  A
69362 CGGCCTTGACGTCTTCGGCGTCGAAGTCCGGGTGGCCGATCGCGAAGGTGTCTGCGGCGTGCACGACGGCGAGGATCCCAGGGACGTCGTCG
          <  A  K  V  D  E  A  D  F  D  P  H  G  I  A  F  T  D  A  A  H  V  V  A  L  I  G  P  V  D  D
69454 AGGGTGGGGCGGCCGCGCCCCAGTCAGCGGGAAGAGTCACGGGGCGATCCTGGCAGCCACCCCGGTCCCGCGCCCCTCATTTTCAACCGC
          <L  T  P  R  R  A  A  W  D  A  P  L  T  V
69545 CCCGCGCCCTGCCCCCGCCGCCGCACGCGCTCGCCGGCGAGAGGGGACCCTTTCTACCCCAGGCGTTAGTAAGGGGCCCTTCCTTGCACCAC
                                                                            <  °  Y  P  A  R  G  Q  V  V
69637 GGCGCGTGCGGTGGTCAGCAGGTCGAGCAGCGCGGTGCCCTCGGCCGGCGTGAGCGCCCGGAATCCGGTCGACACCAGCCGGTCGGTCACCG
          <A  R  A  T  T  L  L  D  L  L  A  T  G  E  A  P  T  L  A  R  F  G  T  S  V  L  R  D  T  V  A
69729 CCTCCGACCACAGCCGGCCGCACCCAGCGGCCCGACCCGGGGGTACGGCGGCGGCCAGCCGCAGGCCAGCGCCCCCGGCCTCCCCCTCCGGC
          <  E  S  W  L  R  R  R  V  L  P  G  V  R  P  Y  P  P  P  W  G  C  A  L  A  G  A  E  G  P
69821 CCGGCCAGCACCGCCTCCAGCGGCGTCATCCCGCCGGCCCGCACCGCCAGCAGGTACGCCCCGGCGAAGTGCTCCCGAAGCAGCAGCAGCCC
          <G  A  L  V  A  E  L  P  T  M  G  G  A  R  V  A  L  L  Y  A  G  A  F  H  E  R  L  L  L  L  G
69913 GGCGGCGGCACGGGCCCCCGGGGTGTCGTCCGGCGGCGGCACGGCCCGCCAGGCGGCAAAGAGTGGCATCCCGCTGGCGTCCGCGGCGTCGA
          <  A  A  A  R  A  G  P  T  D  D  P  P  P  V  A  R  W  A  A  F  L  P  M  G  S  A  D  A  D  V
70005 CCACCCGGTGCAGCAGCGTCGCCAGACGGATCACGCCGGGCACGGCGGTCAGGTGCTCGCTGCCCCACCGGCAGCACTCGGCCAGGTTCGCC
          <  V  R  H  L  L  T  A  L  R  I  V  G  P  V  A  T  L  H  E  S  G  W  R  C  C  E  A  L  N  A
70097 GTGGCCACCTCCAGCGGAGCGTGCACGCGGGCGGCGGCGTCCCCACCCGTCGGCGACCGCGTCGGGGGCGACGAAGCCGAGGGCCGCGCTCAC
          <T  A  V  E  L  P  A  H  V  R  A  A  A  D  W  G  D  A  V  A  D  P  A  V  F  G  L  A  A  S  V
70189 CGTGGCGGCCCCGACGTCGCCGAGCACCCCGGCCCGGCCGGCGATGTGGAAGGCCCAGCCGGAGATGCCCAGCAGACGGGCCCGGTGCAGGG
          <  T  A  A  G  L  V  G  A  R  G  A  I  H  F  A  W  G  S  I  G  L  L  R  A  R  H  L  T
70281 TGGCCGGGCAGCGGGCGAACATCTCCCCGAGCTCCAGCACCAACGGCTTGCTCGCGGCGGCGACCTGCTCCGGCGTCATCGGGTTCAGTCT
          <  A  P  C  R  A  F  M  E  G  L  E  L  V  L  P  K  S  A  A  A  V  Q  E  P  T  M     <  °  D
70372 GCCCCGCCGGGGCCTTCCGTGACAGCCCCGTCTTCGGCGTCGACCGCCTCGATCGCCCCCTCGATTTCGCCGGTGCGGCGCTGGGCGGCGGT
          <A  G  G  P  G  E  T  V  A  G  D  E  A  D  V  A  E  I  A  G  E  I  E  G  T  R  R  Q  A  A  T
70464 GACGGCCCGTTCCGCGCCCGCCGGGCCAGCTTCCGCCGGCTGAGTTCCTGCTCGGCCTCTGCGCGCGATCGCTCCAGGTCGGCCAGCGACC
          <  V  A  R  E  A  A  R  R  A  L  K  R  R  S  L  E  Q  E  A  E  A  R  S  R  E  L  E  A  L  S  R
70556 GCTCGATGCCGGTCAGTTCCTCGGCACCGTCGTGCTCGGCCTCCACCGCGCCGGCCAGCTCCGCCTCGGCCCGCTCCTGGTCGGTACGCGCC
          <  E  I  G  T  L  E  E  A  G  D  H  E  A  E  V  A  G  A  L  E  A  E  A  R  E  Q  D  T  R  A
70648 CGCGCCAGTTCCCGTTCCAGCATCCGGCGTTGCCGGGGCCCGCTCGGCACGGGCGGCGCGCTCGGCCTCCCGGGCGGCCCGCTTCGCGCGCGG
          <R  A  L  E  R  E  L  M  R  R  R  Q  A  R  E  A  R  A  A  R  E  A  E  A  A  R  K  A  R  P
70740 TGGTGGGTGGGTGGGCGGTGGCTGCTCCTCGCCGCCGGTGACCAAACGGAGCTGGGGGCGGGGCACCTCGCCGAAGCGGCGTAGCTGGCGG
          <  P  P  H  T  P  P  P  Q  E  E  G  G  T  V  L  R  L  Q  P  R  P  V  E  G  F  G  A  Y  S  A  A
70832 CCCGCAGCAGCCGGCCGGAGCGCACCTGCCCGGCCACCTCCGTGTCGGAGAGCGCGGCGTCGAGCGTCGCCTCCACCTCGCCCAGCGGCAGC
          <  R  L  L  R  G  S  R  V  Q  G  A  V  E  T  D  S  L  A  A  D  L  T  A  E  V  E  G  L  P  L
70924 TTCCCGGCCGGCGGGCGCCCTCGGCGTCGGCGGCGCAGCCGGCGGCGCCTCGGCGACCAGCGCGGCGACCGCCGCCGCGCTGGGCGGAGAG
          <K  G  A  P  P  G  G  E  A  D  A  A  L  R  R  A  E  A  V  L  A  A  V  A  A  R  R  Q  A  S  L
71016 TTCCCGCAGCCGGGGGCGCGCAGGTCGCGCTGGGCGCGGCGGCAGCGCCTCGGCGAGTTGGGTCAGGTCGGCGACCAGCTCGGGGCGGCGCA
          <  E  R  L  R  P  G  R  L  D  R  Q  A  R  R  L  A  E  A  L  Q  T  L  D  A  V  L  E  P  R  R  L
71108 GGGCGAGCAGGTTGACCAGCCACGCGGCCACGGTCGGGCGGCGCAGCCGGGCGATCTCGCGGGCCGTGGCCGGGTCGCCGGAGCGCCGGGCC
          <  A  L  L  N  V  L  W  A  A  V  T  P  R  R  R  L  R  A  I  E  R  A  T  A  P  D  G  S  R  R  A
71200 TCGGCGACGGCGGCGTCGCGGGTGGCGACGAACTTCTCGGCGGCTCCGGAGGAGGCTCTGCGGGGGCGGCACGGCTC
          <E  A  V  A  A  D  R  T  A  V  F  K  E  P  P  E  T  Y  L  R  R  R  L  L  S  Q  P  P  P  V  <  °
```

Figure 11S

```
71291 AGACGTCGAGCCGGCTGCCCGGCTCGAGGCGCTGGTAGTCGGTCCCCGACAGCGCGGCGTACTGACGGTTGAGGACGGCGAGGCCGTTGTCG
        <  V  D  L  R  S  G  P  E  L  R  Q  Y  D  T  G  S  L  A  A  Y  Q  R  N  L  V  A  L  G  N  D
71383 TTGAGCAGCCCGTCGTGCAGGGCGAAGGCTCGGCGCGGGGCGACCGCGCGGATGAAGTCGAGCACCTCGGAGAACTTCGACCAGGGGCGTG
       <N  L  L  G  D  H  L  A  F  A  R  R  P  A  V  A  R  I  F  D  L  V  E  S  F  K  S  W  P  A  H
71475 GATCGGCGCGAAGAGGGTGTCCACGGGGCGTCCTCGGGTGCCACCAGGGCGTCGCCGGGGTGGTAGACGACGTCGTTCAGCAGATACCCGA
        <  I  P  A  F  L  T  D  V  P  A  D  E  P  A  V  L  A  D  G  P  H  Y  V  V  D  N  L  L  Y  G  L
71567 GGTTGTCCACGACCGGGATGTCGGGATGGATGACGCCGTCGACCGCCGTACGCGCGCACCGCCACGCCGCCGGTGAACGCCTGCCCG
        <  N  D  V  V  P  I  D  P  H  I  V  A  H  R  G  G  Y  A  R  V  A  V  G  A  A  T  F  A  Q  G
71659 GGTGAGATGGGCTCCAGGGCTTCGGCCACGTCGCCGAGGGCACCGGCCAGCGAGGCCGGGCCGTAGATGCGGAACGGCCAGCGGTCGAGCTG
       <P  S  I  P  E  L  A  E  A  V  D  G  L  A  G  A  L  S  A  P  G  Y  I  R  F  P  W  R  D  L  Q
71751 CCGGGTGAGAGCCGGCGACGTCCACGTGGTCGGGGTGCTCATGGGTGATCAGCACCGCGTCCGCACCGTCCAGCGCGGTCGGGTCGCTGAAGA
        <  R  T  L  A  A  V  D  V  H  D  P  H  E  H  T  I  L  V  A  D  A  G  D  L  A  T  P  D  S  F  V
71843 CGCCCGGGTCGACGACCAGCACACCGCCGTCGTGCTCGACGCGGAGGCAGGAGTGGGCGAATTTGGTGAGCTGCATCGTGACTCCTCGAT
        <  G  P  D  V  V  L  V  G  G  D  H  E  V  R  L  C  S  H  A  F  K  T  L  Q  M
71933 TGACCCAATCGTGATGTCCCTCAGCGCAGTCTGCCGGAACCGGCGCGGTGCCGCGTCGCGTCTGAGGTATCGCCCGATGGGGCGTAGACGAT
72025 CGGAGCGGGAATGGACGGACACGCAAGACGCAGGTTGCTGACCGCGGTGGGGCTGGTGGCGCTGCTGGCGGCCGGTGGTTGCAGCGCCGACA
72117 GCGATGGGGCGGGAGAGCCTTCGGCGGCCGGTGGCGCCCGAGCAGGCGGCACCTGCCGACGGGGGCAAGGCGGAGCAGGGTGCCGATGCCGGG
72209 GGAACGCGGTCCGGCGCGGGTGGCGGCTCACCGGACCTGCGGGTCGACCAGCGGTCAATCATCTACACCGGAACCATGCGGGTGCGGGTGG
                                                                                    >  M  R  V  R  V
72300 ACGATGTGGACGCCGCCGCCCGGTCCGCCATCACGGCGGTCACCGGCGTCGGCGGCTTCGTCGGCGGCGACGAGCGCAGCAGCGGCGGAACC
       >D  D  V  D  A  A  A  R  S  A  I  T  A  V  T  G  V  G  G  F  V  G  G  D  E  R  S  S  G  G  T
72392 GCCGACGCCCGGCGGAGTTGCAACTGCGGGTGCCGGCGGAGCGGTTCACGGCCGTCCTGGAGGAGTTGGCGAGGCTCGGCCGGCAGGAGCA
       >  A  D  A  R  A  E  L  Q  L  R  V  P  A  E  R  F  T  A  V  L  E  E  L  A  R  L  G  R  Q  E  Q
72484 GCGGGCGATCCGCACGGAGGACGTGACCGAGGAGACCGTGGATCTCGACGCGGATCGCCACCCAACGGGCCCGGGTCGAGAGCGGGTCGCA
       >  R  A  I  R  T  E  D  V  T  E  E  T  V  D  L  D  A  R  I  A  T  Q  R  A  R  V  E  S  G  R
72576 AGCTGCTGGCGCGGGCCACCTCGATCGGCGACCTGGTGACGCTGGAGAGCGAGGTGGCTAGGCGGGAGGCCGACCTCGCCTCGCTGGAGGCG
       >K  L  L  A  R  A  T  S  I  G  D  L  V  T  L  E  S  E  V  A  R  R  E  A  D  L  A  S  L  E  A
72668 AAGAAGCGCCGGCTGGCCGACCTGACCTCGCTCTCCACCATCACCCTCACCCTGGTCGGTCCGGAAGGCGGAGGCCCGGGACACCGAGCCCGA
       >  K  K  R  R  L  A  D  L  T  S  L  S  T  I  T  L  T  L  V  G  P  E  A  E  A  R  D  T  E  P  D
72760 CACCGGCTTCGTGGTCGGCCTGCGCGGCGGCTGGACGGCGTTCGTCGCCTCGCTGGGCGTGCTGCTCACCGTGCTCGGGGCGCTGCTGCCGT
       >  T  G  F  V  V  G  L  R  G  G  W  T  A  F  V  A  S  L  G  V  L  L  T  V  L  G  A  L  L  P
72852 TCGCGGTGGCCCTCGGCGTGCCGGTGGCGGTGCTGCTTGCGGTGCTGCGGCGGCGCCGGCGTCGACCGCCGGCGCCGGCCGTCAACGCGCC
       >F  A  V  A  L  G  V  P  V  A  V  L  L  A  V  L  R  R  R  R  R  R  P  P  A  P  A  V  N  A  P
                                                                                        <  ∘  R  A
72943 GCCGCCAGTGCCCGCAGCGCGGTCTGCACCATGACCCGGATGCCGACCGCGATGGCCCCCTCGTCGACGTCGAACGAGGCCCGGTGCAGGT
       >  P  P  V  P  A  A  R  S  A  P  ∘
       <A  A  L  A  R  L  A  T  Q  V  M  V  R  I  G  V  A  I  A  G  E  D  V  D  F  S  A  R  H  L  D
73034 CGACGTTCGGGCCGGACCGGCCGACGCCGAGGCGGGCCAGCGCGCCGGGGACGTACTCCAGGTACCAGGAGAAGTCCTCGCCGCCCATGCTC
       <  V  N  P  G  S  R  G  V  G  L  R  A  L  A  G  P  V  Y  E  L  Y  W  S  F  D  E  G  G  M  S
73126 TGCGGGGTCTCCGCGACCCCCTCCGGGCCGAGCGCGGCGTGGGTCGCCGCGTGAGCACCTGGATCGCCGGGCGTCGTTGGTCACCGGCGCG
       <Q  P  T  E  A  V  G  E  P  G  L  A  A  H  T  A  A  T  L  V  Q  I  A  R  A  D  N  T  V  P  P
73218 CCGGCCGCGTAGGTACTCCAGGTCGACGGTGGCGCCGGTGGGGGCGATGACGTCCCGCACCACCTGAGCGACGATCTTGGGGGCCTGGTCCC
       <  R  G  R  L  Y  E  L  D  V  T  A  G  T  P  A  I  V  D  R  V  V  Q  A  V  I  K  P  A  Q  D  W
73310 AGGTGTCGCGGTCCATCACCCGCAGGGTGCCGGACGGCGAGCGCCTCGGACGGGATCACGTTGTACCGGGTGCCGGCCGAGGCGTGGCCGAAC
       <  T  D  R  D  M  V  R  L  T  G  S  A  S  A  E  S  P  I  V  N  Y  R  T  G  A  S  A  H  G  F
73402 ACGAGCAGCAGCCCGCTGTTGGCCGGCACCCGGCGGCTGACCAGGGCTGGCACCTCGGTGACCAGCCGCGAGCCGTCGACCAGGTCGAC
       <V  L  L  L  G  S  N  A  P  V  R  R  S  V  L  A  P  V  E  T  V  L  R  G  L  A  D  V  L  D  V
73494 GGTCAGGTGCGGGCGAGCGGTGTGCCCGCCGGGGCCGGTGAGCCGGACGGTGACGTTGTCGGCGGCGGCGGTGATCGGGCCGACCCGCAGGC
       <  T  L  H  P  R  A  T  H  G  G  P  G  T  L  R  V  T  V  N  D  A  A  A  T  I  P  G  V  R  L  G
73586 CGACCTTGCCGACGGGCTGGTTGGGGTCGCAGTGCAGTGCGAAGATCTGCACGACGTCGTCGAGACCGCCGGCCTCGATGACCTCCAGCGAG
       <  V  K  G  V  P  Q  N  P  D  C  H  L  A  F  I  Q  V  V  D  D  L  G  G  A  E  I  V  E  L  S
73678 CCGCAGGGCAGGATCTCCTCGGCCGGCTGGAAGATCAGCCGGACCCGGCCGTCCAATTCGCCGAGGTTGGCGAGTTGGGCCAGCAGCACGCC
       <G  C  P  L  I  E  E  A  P  Q  F  I  L  R  V  R  G  D  L  E  G  L  N  A  L  Q  A  L  L  V  G
73770 GACGCCGAGCAGCACGTGGTGTGCACGTCGTGGCCGCAGGCGTGGCAGACACCGTCCTTGGTGGACCGGTAGGGCACGTCCTTGACGTCGG
       <  V  G  L  L  V  T  T  H  V  D  H  G  C  A  H  C  V  G  D  K  T  S  R  Y  P  V  D  K  V  D  T
73862 TCAGCGGCAGCGCGTCGATGTCGGCGCGGAGCGGCGACCACCGGGCCGTCGGGGCGGCGTCGATGTCGCAGATGACCCCGTTGCCCTTTGGC
       <  L  P  L  A  D  I  D  A  R  L  A  V  V  P  G  D  P  R  G  D  I  D  C  I  V  G  N  K  P
73954 AGCAGGCGCGGGCGCAACCCGGCGAGCGACAGCTCGCGGGCGATCAGGGCGCCGTCTCGAACTCCTCGCCGGAGAGCTCCGGGTGGGAGTG
       <L  L  R  P  R  L  G  A  L  S  L  E  R  A  I  L  A  A  T  E  F  E  E  G  S  L  E  P  H  S  H
74046 GATGTGCCGGCGGGTGGCGATAAGGCCGGGCATCCGGAGGGCGAGCAGATGGTCGAGCTCGAAGGGCAAAGGCTGCGACCCGGACGGCGACT
       <  I  H  R  R  T  A  I  L  G  P  M  R  L  A  L  L  H  D  L  E  F  P  L  P  Q  S  G  S  P  S  E
74138 CCGGCCAGGCCGACGACGCCAGGTGGCTGCCGTTCGGCAGCGTCAACGCACTCGTCACGTCGAAATCTCGATCACTAGAAACGGATGGATC
       <  P  W  A  S  S  A  L  H  S  G  N  P  L  T  L  A  S  T  V
74229 ATCAGGGATGACAGCCGCCAGCCTAGACCTTCGACGGTGACTCTGTGCAACATCATTCCCGTAGCGATCGGACCGCGCAGCGTCACGAATAC
74321 CCTGGTGGAAGGGCTCCATAATCTGCGGGACAGCAGGTAGATCGCGGTTGAACGCCGTCATCTGCCCCCCACCTCCTACAACCCGTAACCGA
74413 TTCGGCGGTCACGAAATCACCGTCGATCCGGGGCGTCGCTACCGAATTGTCGCATTAGTCGTTCGGTTAACTGCCGCTCGGACAAGTAAC
74505 CGACCGCACTCGGCAGTCGGACGACTCCCGACGGTGACACGAGGGCCGACCTGCTCCCGCACATGCTGTCCGTCCCAATCACCCGGACGGGCC
74597 TTACCCACTGCCCCGGGTGGCACACACCGGGCTGCCCCGGGTGGCACACACCGGGCTGCCCCGGGTGGCAGGGTGCCACAGACCTCGCCCACCGTGGCC
74689 CTCATCCGAGACAAGGGGTCAGAACCGGTCGCTGGGCGGTACGTCCCCCACACCTGGCGCAGGGTGCCACAGACCTCGCCCACCGTGGCC
                < ∘  F  R  D  S  P  R  Y  T  G  W  V  Q  R  L  T  G  C  V  E  G  V  T  A
74780 CGGGCCCGCAGCGCCTCCTTCATCGGGTGCAGCACGTTCGCCGTACCCTCGGCGGCGGCCCCGCAGCTCACCCAGCGCGCGCTCGACGGCGTC
       <R  A  R  L  A  E  K  M  P  H  L  V  N  A  T  G  E  A  A  A  R  L  E  G  L  A  R  E  V  A  D
74872 GCTGTCGCGCTCCACTCGCAGCTTGGCCAGCCGCTCGGCCTGGGCAGCCTCGATCGTCGGGTCCACCCGCAGCGGCTCGTACGGCTCGTCGG
       <  S  D  R  E  V  R  L  K  A  L  R  E  A  Q  A  A  E  I  T  P  D  V  R  L  P  E  Y  P  E  D  A
74964 CGTCGACCGTGAACCGGTTGAGGCCGACCACCACCCGCTCGCCCGAGTCGATCTCCTGGGCGATCCGGTACGCGGACTGCTCGATCTCCCGC
       <  D  V  T  F  R  N  L  G  V  V  V  R  E  G  S  D  I  E  Q  A  I  R  Y  A  S  Q  E  I  E  R
75056 TTCTGGAAGCCCGCCTCGATGGCGTCGACCACCGAGCCGTGGTCGGCGCACCCGCTCCATCAGCTCCACCACCGCCGCCTCGATCTCGGCGGT
       <K  Q  F  G  A  E  I  A  D  V  V  S  G  H  D  A  V  R  E  M  L  E  V  V  A  A  E  I  E  A  T
```

Figure 11T

```
75148 CATCGCCTCCACCACGTACGACCCGGCGAACGGGTCGACGGTGGCGGTCAGGTCCGTCTCGTACGCGAGCACCTGCTGGGTGCGCAGCGCCA
         <  M  A  E  V  V  Y  S  G  A  F  P  D  V  T  A  T  L  D  T  E  Y  A  L  V  Q  Q  T  R  L  A  L
75240 GCCGGGCGGCCTTCTCGGTGGGCAGCGCGATGGCCTCGTCGAAGCTGTTCGTGTGTAGCGACTGGGTGCCGCCGAGCACCGCGCCCAGCCCC
         <  R  A  A  K  E  T  P  L  A  I  A  E  D  F  S  N  T  H  L  S  Q  T  G  G  L  V  A  G  L  G
75332 TGGATCGCGCCACCCGGACCAGGTTCACCTCGGGCTGCTGGGCGGTGAGCTGCACGCCCGCCGTCTGGGTGTGGAAGCGCAGCATCATCGACTT
         <Q  I  A  V  R  V  L  N  V  E  P  Q  Q  A  T  L  Q  V  G  A  T  Q  T  H  F  R  L  M  M  S  K
75424 CGGGGTTCTTCGCGCCGAACTCGTCGCGCATCAGCCGGGCCCAGATCGCGGGCGGCACGGAACTTCGCGACCTCCTCCAGCAGGGTGGTCC
         <  P  N  K  A  G  F  E  D  R  M  L  R  A  W  I  R  R  A  A  R  F  K  A  V  E  E  L  L  T  T  R
75516 GGGCGACGAAGAAGAACGACAGCCGGGGCGCGAAGTCGTCCACCGCCAGCCCGGCGGCGAGCGCGGCCCGGACGTACTCGACGCCGTTGGCC
         <  A  V  F  F  F  S  L  R  P  A  F  D  D  V  A  L  G  A  A  L  A  A  R  V  Y  E  V  G  N  A
75608 AGCGTGAACGCGATCTCCTGCGCGGGCGACGCCCGGCCTCGGCCATGTGGTAGCCGGAGATGGAGATGGTGTTCCACTTCGGCACCTCCGC
         <L  T  F  A  I  E  Q  A  P  S  A  G  A  E  A  M  H  Y  G  S  I  S  I  T  N  W  K  P  V  E  A
75700 CCGGCAGTAGGCGAACGTGTCGGCGACCAGCCGCAGCGAGGGCTTCGGCGGGAAGATGTACGTGCCCCGGGCGATGTACTCCTTGAGGATGT
         <  R  C  Y  A  F  T  D  A  V  L  R  L  S  P  K  P  P  F  I  Y  T  G  R  A  I  Y  E  K  L  I  D
75792 CGTTCTGGATGGTGCCGTTGAGCGCCGCGCCCGGCACCCCCGCCTCCTCGGCGACGAGCTGGTAGAGCAGCAGCAGCACCGACCCCGGGGCG
         <  N  Q  I  T  G  N  L  A  A  G  P  V  G  A  E  E  A  V  L  Q  Y  L  L  L  L  V  S  G  P  A
75884 TTGATCGTCATCGAGGTGGAAACCTTGTCCAACGGGATGCCGTGGAACAGCAGCAGCCGCATGTCCTCGATCGAGTCGATGGCGACGCCGACCTT
         <N  I  T  M  S  T  S  V  K  D  L  P  I  G  H  F  L  L  R  M  D  E  I  S  D  I  A  V  G  V  K
75976 GCCGACCTCGCCGTGGGCGATCGGGTCGTCCGAGTCGTACCCCATCTGGGTGGGCAGATCAAAAGCGACGGAGAGGCCCATGGTGCCGGCGC
         <  G  V  E  G  H  A  I  P  D  D  S  D  Y  G  M  Q  T  P  L  D  F  A  V  S  L  G  M  T  G  A  R
76068 GCAGGAGCTGGTGGTAGCGCGCGTTGCTCTCCGTCGCGGTGCCGAAGCCGGCGTACTGGCGCATCGTCCACGGCCGCGAGGTGTACATGGTG
         <  L  L  Q  H  Y  R  A  N  S  E  T  A  T  G  F  G  A  Y  Q  R  M  T  W  P  R  S  T  Y  M  T
76160 GAGTAGACCCCACGGGTGTACGGGAACTCCCCCGGCTCGCCCAGCCGCTCGGGCAGACCCTCCGCAGGTCCCTCTGGGTGTAGACACCCTT
         <S  Y  V  G  R  T  Y  P  F  E  G  P  E  G  L  R  E  P  L  G  E  P  L  D  R  Q  T  Y  V  G  K
76252 GATCGGGAAGCCGGACTCGCTCGACCGCGGTTCACTCATCCCCGGATGGTAGGACGTGCCACCGCGCCGGAGGGTGAGGGATTGCGCACAT
         <  I  P  F  G  S  E  S  S  R  P  E  S  M
76343 CGCACCCCTGTCTTTCCCCGCCGACTCCGAGGGTGAACACCTGGCCACGTTCGCTCCGATTAGGTAAACGTTCCGCCGCGTCGGGTTTCGCA
76435 TCGGGCGTCGGAACCAGCAAGATAGAGGAGTTGTGTCCCAGCCCCTCGATTTCCCCGGTGGCTCTTCTGTGACTCAGATCCCGACGTGGA
76527 GCGGCGGACCAGTCAGCCCACCCCACGGACGTGCGGCGACCGGCACCACCATCGGTGACCGGTACTCGCTCCGGTCCGCGGTGGGCAATGGC
76619 GGCATGGGCACGGTCTGGCGTGCCACAGACACCCTGCTGCGGCGCGACGTGGCGGTGAAGGAGGTCCTCCCGCCCGGCCTCGCCCCGA
         >  M  G  T  V  W  R  A  T  D  T  L  L  R  R  D  V  A  V  K  E  V  V  L  P  P  G  L  A  P
76710 GCGACCGCGACGCCATGTACGAACGCACGCTGCGCGAGGCCCGCGCGGCGGCGGCCATCCAGCACCCGGCCGTGGTCCAGGTGTACGACGTG
         >S  D  R  D  A  M  Y  E  R  T  L  R  E  A  R  A  A  A  A  I  Q  H  P  A  V  V  Q  V  Y  D  V
76802 GTCACCGAGGGTGGTCGCCCCTGGATCGTGATGGAGCTGCTGGACGCCCGCAGCCTGGCCGACATGGTGATCGAGGACGGGCCGGTGGCCCC
         >  V  T  E  G  G  R  P  W  I  V  M  E  L  L  D  A  R  S  L  A  D  M  V  I  E  D  G  P  V  A  P
76894 CCGCGCGGTCGCCAAGATCGGCATCGCCCTGCTCGGCGCGCTGGAGGTGGCCCACGCGATCGGGGTGCTGCACCGCGACGTGAAGCCGGCCA
         >  R  A  V  A  K  I  G  I  A  L  L  G  A  L  E  V  A  H  A  I  G  V  L  H  R  D  V  K  P  A
76986 ACGTGCTGATCTGCACCGACGGCCGGTGCGTGCTGACCGACTTCGGGGTGGCCAAGCTCCCCACCGACGTGCAGCTCACCACGCCGGGGATG
         >N  V  L  I  C  T  D  G  R  C  V  L  T  D  F  G  V  A  K  L  P  T  D  V  Q  L  T  T  P  G  M
77078 GTGCTCGGCTCGCCGCACTTCATCTCCCCCGAGCGGGCCATGGGCCAGGAGTTCGGCCCGCCGAGCGACCTGTTCTCCCTCGGCGTCACGCT
         >  V  L  G  S  P  H  F  I  S  P  E  R  A  M  G  Q  E  F  G  P  P  S  D  L  F  S  L  G  V  T  L
77170 CTACACGGCGGTGGAGGGCCGGCCCCCGTTCGACAGGGGCGACCCGATCGAGACCATGCACGCCGTGGTCGAGGACCCGCCGGCCACGCCGC
         >  Y  T  A  V  E  G  R  P  P  F  D  R  G  D  P  I  E  T  M  H  A  V  V  E  D  P  P  A  T  P
77262 AGCGCAGCGGCCCGCTGACCCGGGTGCTGATGGGGCTGCTGGAGAAGGACCCGGCCCGCCGCCTCGACGTGCACACCGCCCGCGCGATGCTC
         >Q  R  S  G  P  L  T  R  V  L  M  G  L  L  E  K  D  P  A  R  R  L  D  V  H  T  A  R  A  M  L
77354 CGCGAGCTGCTCGCCGGCCCGCTGACCAGCACCGCCACCGCCGTCAACTCGGTCACCGACCCGTACGCGGTGGTGCCGGTCAAGCAGCGCCC
         >  R  E  L  L  A  G  P  L  T  S  T  A  T  A  V  N  S  V  T  D  P  Y  A  V  V  P  V  K  Q  R  P
77446 GGCCGTCGCCCCACCGCCCTCCGCTGCGGAGCCGAAGCCGAGCGGGCAGATCGGCGGCCGGGCGATGCTCGCCCCCGGCGAGTCGCTGACCG
         >  A  V  A  P  P  S  A  A  E  P  K  P  S  G  Q  I  G  G  R  A  M  L  A  P  G  E  S  L  T
77538 ACCGGCTGGCGGCCCTGCGCCGGGGCGAGAAGACGAGGAAGAGGAAGACGACGACCGCCGCCCGCTGGACGACACCAGCGCCGACGCGCTT
         >D  R  L  A  A  L  R  R  G  E  K  T  R  K  R  K  T  T  T  A  A  A  L  D  D  T  S  A  D  A  L
77630 GCCGGCCCGCTGCACACCCCCACCGGGGCGATGCCCGCGCCCCCGCCCGCCGGCCGGACGTACGGCGGTTCGTCGGAGGCCACCCAGCGGGT
         >  A  G  P  L  H  T  P  T  G  A  M  P  A  P  P  P  A  G  R  T  Y  G  G  S  S  E  A  T  Q  R  V
77722 CGACGGGGGACCGCGCCGGAGGGCCACCCAGCGGATGACGTACGGCAGCCCGCCCGACGCCACCCAGCGGGTGTCCCACGGGAGCGGCCCGT
         >  D  A  G  T  A  P  E  A  T  Q  R  M  T  Y  G  S  P  P  D  A  T  Q  R  V  S  H  G  S  G  P
77814 CGGAGGCCACCCAGCGGGTGCCCTACGGCGGCGGCTCGGCGGACGCCACCCAGCAGGTGCCCTTCGGTCGCCGGCCCGACGCGAGCGG
         >S  E  A  T  Q  R  V  P  Y  G  G  G  S  A  D  A  T  Q  Q  V  P  F  G  R  R  P  D  A  T  Q  R
77906 GTCCCCTACGGCAGCCAGCCCGGCGCGACGCAGCCGGTCCCCGGCTTCGGCGCGTCGCCGGACGCCACCCAGCGGGTCGGCGGGGCGTACGG
         >  V  P  Y  G  S  Q  P  G  A  T  Q  P  V  P  G  F  G  A  S  P  D  A  T  Q  R  V  G  G  A  Y  G
77998 CGGCGGCCAGTGGTCGGTGCCCGGCACCGGCCAGCCGTGGGCCACCCCGGCCACCGCGCCCCCGGCCACCGCCGGCGGCGGCGGGGTCG
         >  G  G  Q  W  S  V  P  G  T  G  Q  P  W  A  T  P  A  T  A  P  A  T  A  G  G  G  V
78090 GCCGCCTCGTCGCCACGGTCAAGGGCTGGCCGCGCAAGGTGCAGCTCGCCGGCCGGCGGCGTCGCCGTGCTGCTGCTGATCGGCGTGTTC
         >G  R  L  V  A  T  V  K  G  W  P  R  K  V  Q  L  A  A  A  G  G  V  A  V  L  L  L  I  G  V  F
78182 GCCCTCTTCGGCGGCGACGACCCGGAGCAGCCGACCACCCCGCAGGGGCAGCCGAGCGCCGGGGCGCCCGCCGGCCCCGGGGTGGAGATGCA
         >  A  L  F  G  G  D  D  P  E  Q  P  T  T  P  Q  G  Q  P  S  A  G  A  P  A  G  P  G  V  E  M  Q
78274 GGAGCAGTCGGCCAAGGGCGTCACGGTGCAGGTGCCCAAGGGCTGGGAGCGGCGCAGTGCCGACGGGGGCGTGTGGGTCGACTACATCGATC
         >  E  Q  S  A  K  G  V  T  V  Q  V  P  K  G  W  E  R  R  S  A  D  G  G  V  W  V  D  Y  I  D
78366 CGGAGGACAACAGCCGCAAGGTGCGCATCCTCGCCGAGCGGTGGAGCGGCACGTCGACGCGCTGGGCCGAGACCGCCGCGAACGGGCTGCGG
         >P  E  D  N  S  R  K  V  R  I  L  A  E  R  W  S  G  T  S  T  R  W  A  E  T  A  A  N  G  L  R
78458 ACCCGGTCGGCCTCCTGCCAGAAGCCGTACAACCAGGTGTCGATGACCGAGCAGGAGCTCGACGGCAAGGCGGCGGCCGAGTTCGAGTACAC
         >  T  R  S  A  S  C  Q  K  P  Y  N  Q  V  S  M  T  E  Q  E  L  D  G  K  A  A  A  E  F  E  Y  T
78550 CTGCGGCGACGGCGAGGGCAAGCGGCACGGCGTGTGGCGCGGGGTGGTGCACGAGGGCAAGGTCTACTCGTTCTACCTCTCCTCGACCGACG
         >  C  G  D  G  E  G  K  R  H  G  V  W  R  G  V  V  H  E  G  K  V  Y  S  F  Y  L  S  S  T  D
78642 CCCGCTTCGCCGAGAGCAAGCCGATCTTCGATCAGATGGTGGCGTCGTTCAAGCTCCGCGGGAGCGACTGAGCCGGGCCGGGGGCCGACGC
         >A  R  F  A  E  S  K  P  I  F  D  Q  M  V  A  S  F  K  L  R  G  S  D  •
78733 GACGCCGGCCGGGCGGGCCGACGCGACGTGGTGAGCCGCCGCCGTGCTATCAAGAGCCATGGCGGCGGACACCACTGACCTCGACGACACG
                                                                            >  M  A  A  D  T  T  D  L  D  D  T
78824 CGCGATCTGGACGACCTTCGCGACCGGGCCCGGCGGTGGCTCGACGACGACCCCGACCCGGACGCGACGAGTGGAGGCCGTGCTCGA
         >  R  D  L  D  D  L  R  D  R  A  R  R  W  L  D  D  D  P  D  P  A  T  R  D  E  L  E  A  V  L  D
```

Figure 11U

```
78916 CGGGCTGCCGGCGAGCGCGGCCGAGCTGGCCGACCGGTTCGCCGGGCCACTGACCTTCGGCACCGCCGGGCTGCGCGGCCCGCTGCGCGCCG
         >  G  L  P  A  S  A  A  E  L  A  D  R  F  A  G  P  L  T  F  G  T  A  G  L  R  G  P  L  R  A
79008 GCCCCAACGGGATGAACCTCGCCGTGGTCACCCAGGCCGCCGCCGGGCTCGTCGCCTGGCTCGCCGCCCAGGACGCCACCGGGCCGCTGGTC
        >G  P  N  G  M  N  L  A  V  V  T  Q  A  A  A  G  L  V  A  W  L  A  A  Q  D  A  T  G  P  L  V
79100 ATCGGGTACGACGCCCGGCACGGCTCGCGGGAGTTCGCCGAGCGCACCGCCCAGGTGGCCACCGGCGCGGGCCGCCCGGCGCTGCTGCTGCC
         >  I  G  Y  D  A  R  H  G  S  R  E  F  A  E  R  T  A  Q  V  A  T  G  A  G  R  P  A  L  L  L  P
79192 CCGCCCGCTGCCCACCCCCGTGCTGGCGTACGCGGTGCGGCAGTCGACGGCGGCCGCCGGCGTGATGGTGACCGCCAGCCACAACCCGCCC
         >  R  P  L  P  T  P  V  L  A  Y  A  V  R  Q  L  D  A  A  A  G  V  M  V  T  A  S  H  N  P  P
79284 AGGACAACGGCTACAAGGTCTACCTCGGCGCGCAGCTCGGCGGCGAGCTGGGCGCGGGGGCGCAGATCGTGCCGCCGGCCGACACCGGCATC
        >Q  D  N  G  Y  K  V  Y  L  G  A  Q  L  G  G  E  L  G  A  G  A  Q  I  V  P  P  A  D  T  G  I
79376 GAGGCCGCCATCCGGGCGGTCGGCCCGCTGGCCGACGTACCGCTGGGCCCGGCCGGGCAGGTCGTCGGCGACGACGTGGTCGTGTCGTACGT
         >  E  A  A  I  R  A  V  G  P  L  A  D  V  P  L  G  P  A  G  Q  V  V  G  D  D  V  V  V  S  Y  V
79468 CGACCGGGCCGCCGCCGTGGTCGACCCGGCGGGGCCCCGGAGCCTGAAGGTGGCCTACACGCCGCTGCACGGCGTGGGCGCGGCCGTGCTGA
         >  D  R  A  A  A  V  V  D  P  A  G  P  R  S  L  K  V  A  Y  T  P  L  H  G  V  G  A  A  V  L
79560 CCGCCGCCTTCGCCCGCGCCGGCTTCGGCATCCCCGGCGTGGTGCCCGAGCAGGCGGTGCCGGACCCGGACTTCCGGACCGTCAGCTTCCCC
         >T  A  A  F  A  R  A  G  F  G  I  P  G  V  V  P  E  Q  A  V  P  D  P  D  F  R  T  V  S  F  P
79652 AACCCCGAGGAGCCGGGGGCGGGTGGACCTCGTCGCGCTCGCCGAGCGCACCGGGGCGGACCTGGCGATCGCCAACGACCCCGACGCGGA
         >  N  P  E  E  P  G  A  V  D  L  L  V  A  L  A  E  R  T  G  A  D  L  A  I  A  N  D  P  D  A  D
79744 CCGCTGCGCGGTGGCCGTCCGCGACGGCCGGGCGGCGGGCCCGGCACCGGTGAGTGGGGGCGCCTGGCGGATGCTGCGCGGGGACGAGGTGG
         >  R  C  A  V  A  V  R  D  G  R  A  A  G  P  A  P  V  S  G  G  A  W  R  M  L  R  G  D  E  V
79836 GGGCGCTGCTCGCCGACCATCTCATGCGCCGTGGCGTCCACGGCCTGTACGCCACCACCATCGTGTCGTCGTCCCTGCTACGGGCCATGTGC
         >G  A  L  L  A  D  H  L  M  R  R  G  V  H  G  L  Y  A  T  T  I  V  S  S  S  L  L  R  A  M  C
79928 GCCGCCCGTGGCCTGCCGTACGACGAGACGCTGACCGGCTTCAAGTGGATCGTCCGGGCCGGCGGCGGGACCGCTGGGTGAGGCCGGCTCCGA
         >  A  A  R  G  L  P  Y  D  E  T  L  T  G  F  K  W  I  V  R  A  G  G  G  P  L  G  E  A  G  S  D
80020 CCCGCTGGTCTTCGGCTACGAGGAGGCGCTGGGCTACTGCGTCGCCCCGGAGCACGTCCGCGACAAGGACGGCATCACCGCCGCGCTGACCG
         >  P  L  V  F  G  Y  E  E  A  L  G  Y  C  V  A  P  E  H  V  R  D  K  D  G  I  T  A  A  L  T
80112 TCGCCGAGCTGGCCGCCGGGCTGAAGGCGCAGGGGCGCACCCTCACCGACCGGCTCGACGAGCTGGCCGCCGAGTTCGGCGTGCACCACACC
         >V  A  E  L  A  A  G  L  K  A  Q  G  R  T  L  T  D  R  L  D  E  L  A  A  E  F  G  V  H  H  T
80204 GACCAACTCTCGGTGCGGGTGGACGACCTGCGCATCATCGCCGACGCGATGGCCCGGGTCCGGGCGGCCACCCCGACGACCCTGCTCGGCCG
         >  D  Q  L  S  V  R  V  D  D  L  R  I  I  A  D  A  M  A  R  V  R  A  A  T  P  T  T  L  L  G  R
80296 CCCGGTGACCGAGGCGCGGGACCTGCTCCCCGAGGCGGACGTGGTGATCCTGCGTACCGACGGGGCACGGGTGGTGATCCGCCCGTCGGGCA
         >  P  V  T  E  A  R  D  L  L  P  E  A  D  V  V  I  L  R  T  D  G  A  R  V  V  I  R  P  S  G
80388 CCGAGCCGAAGCTCAAGGCGTACCTGGAGGTGGTGGAGCCGGTGGCCGGACGGCGACGTGCCGGCGGCCCCGGACGCGCGCGGCGGCCACGCTG
         >T  E  P  K  L  K  A  Y  L  E  V  V  E  P  V  A  D  G  D  V  P  A  A  R  T  R  A  A  A  T  L
80480 GCGGCACTCCGCACGGAAATCGCCGCCCTGGTGCAGGGATGAGGTGTGCTCCCGCTTCCGACGCTCTCTCAGCGGGTTGGCGTGTCGCCCC
         >A  A  L  R  T  E  I  A  A  L  V  Q  G  •
80571 CAGGTTCGTGGTGATATGCGGCCAGGTAAGCCACCGTCCTGCCACTATCCATGTCGTAGAACATGATGCGTGCCACTTGGATGTAGTAGTAG
80663 GTGACCAATGAGGTGAACCCGGGGCCCTGTTTGAGCGTGTACGTAGCGCCGAAGCCACTGGCAGTCACATCGTCACGGCGGGCTTTCCCGTT
80755 AGCGCTCGCGTAGCTCAGCGCAGCAGGAACATCCTCCCCGCCCATAGGGATACAGCAGCTGGCTGGTGTATCCCTTCTCGAAGGGCTTTGCAG
80847 GTTCTGCCGGCAAGGGCGAGAGGTCCTGGGCGTCCGTCTTGATCACGATCTCGTAGAGCCGGACATCGGCCGTCTCGGTGTTGTACGCCAGG
80939 ATGACCGGCACCGGCAAGGTGTTTGGGAGCGTGACCGAAATGGACGTGAACCCGGGTCCGGGGCGCTGCGTCGGCCGCTGCCGGCTTGGGT
81031 GGCGGGCCCGTCCGAGGAATAACTACGGAACATGCAACTGCCGTCTGTCTTGTTGTACAGGAACAGCCACTGCCGCTTTCCACCCTCGCCGT
81123 TCACCTCGAAGGGCGCTACGACGACCATCCAGCGCCCCAGTTGTCCTTCTGGCCATCAGGCGGCCACACCTGCTCGCAACCGTCTTCGTTG
81215 TCCACAACCTGCCACACGGCGCTGTTGCCGGTAAGGGCATCGTAGAGCTGGACATACCGCCTGTCGTTCTGCACGACGGGAACGACGGAGGT
81307 CCACCCCTTCCCGAAATTGCGCTGGTGGGGGAGGCCACTCGGGTGGCATCTCGTCGTGGCATTGACTGGGACCGAAGGCGGCCGTGCCGT
81399 CATTGCTGTTGTAGAACAGCACCGCTGGGCCACTGTAGTGCCCGTCGAAATGCAGAGATATGACGTGCGTGAACCTGGTCCGAGTTGGACA
81491 TCATAGAGCATTCCGGAGTGACATGGGTTTACCCCGTCCTAGGGATCACTGCTTCTCAACAAGATCATCAACGGTGTGCGGCAGGCTGCA
81583 CAATCGGGTGGAAGAAGAGCCAGCACCGGGCCTCACTGGCCATCACAGTATCGTCTGACCTCTTCGACCGGGCCCGAAACGGGCGAACCGAG
81675 AGCGTTCCGCGCATCTGTCGGTCGGGCGTGTCGAAGGTGCGGCTGTTCGCCACGTGCGCGGCGGAGCAGGGTGCCCTCCGCGCCGTCACGGGT
81767 TCTGCCACGAGGCGGCCAGGACCCAGACGTGACCAGCCGGCCATCAGGTTCACGATGAACCGCTTGCGACCGCTGGCTGCGCGCCGCTC
81859 CGGCGGCCCTCCGCGCCGGACCCGGGAACGCGGCACGCTCACCCGCGTGATCCCTTGCCCACGAAGGGCTCGTCTGAATAGCATCAGCACAT
81951 CAGGCCCCACCATTACCCGGCACCATTGGCATTCGCTTTCTTCGACGTTGCGGCTGCGGTGCCCGGGCGTTGCATTTCCGGCGGAAAGGTGT
82043 TGCACGGTGCGTGAAACAAATGGCTCGACCGTGCCGCGACGGCAGCTCGGCAGGCTGCTCACCCAGCTCCGCGAGAGCGCCCATATCAGCA
                                    >  V  P  R  R  Q  L  G  R  L  L  T  Q  L  R  E  S  A  H  I  S
82134 TCGACGCGGCGGCCGGCGAGCTGGACTGCTCGCGGCGACAAGCTCTGGCGGATCGAGCGGGGGCTGACCTCGGCCAAGACACCGGACGTCCGG
        >I  D  A  A  A  G  E  L  D  C  S  R  Q  K  L  R  I  E  R  G  L  T  S  A  K  T  P  D  V  R
82226 GTGCTCTGCGAGCTGTACCGGGCCACGCCCGACCAGGCGAGCGTGCTGCTCGGGCTCGCCGAGGTGAGCCGCGAGGGGTGGTGGCACGC
         >  V  L  C  E  L  Y  R  A  T  P  D  Q  A  S  V  L  L  G  L  A  E  V  S  R  A  E  G  W  W  H  A
82318 CCACGGCAGCTCCGTGCCGGCCTGGTTCTCGCTCTACGTCGGCCTGGAGAACGTCGCGAGCAGCATTCGGCACTACAACGCGGAGCTGGTGC
         >  H  G  S  S  V  P  A  W  F  S  L  Y  V  G  L  E  N  V  A  S  S  I  R  H  Y  N  A  E  L  V
82410 CGGGGCTGTTGCAGACCCCCGGCTACGCCACCGCGCTCTTCGAGCACAACCGGCCCGAGCTGGGCGAGGAGGAGCGAAAGAAGGCGGTGGGC
        >P  G  L  L  Q  T  P  G  Y  A  T  A  L  F  E  H  N  R  P  E  L  G  E  E  E  R  K  K  A  V  G
82502 TTCCGGACTCAGCGGCAGGGGCTGCTGGCCCGGCGGCTGCCCCCGGCCCCCGAGCTGACCGTGATCCTCAGCGAGGCGGTGCTGCGCCGCCC
         >  F  R  T  Q  R  Q  G  L  L  A  R  R  L  P  P  A  P  E  L  T  V  I  L  S  E  A  V  L  R  R  P
82594 GGTGCCGGGCCGATCGGTGATGGCCGACCAGCTCCGGCACCTGCTGGCCGTCGGCGAACGGCACAACATCACCGTACGGGTGCTGCCGCTGG
         >  V  P  G  R  S  V  M  A  D  Q  L  R  H  L  L  A  V  G  E  R  H  N  I  T  V  R  V  L  P  L
82686 CCGCCGGGCCGCCGCTGGCCGCGGAGGCGGCACGTTCGTGCTGCTCGACTTCCCGCTCTCGGCGCTCGGCAGCCCGACCGAGCCGCCGACC
        >A  A  G  P  P  L  A  A  E  A  G  T  F  V  L  L  D  F  P  L  S  A  L  G  S  P  T  E  P  P  T
82778 GTCTACGTCGAGGGGCTCACCGGCGCGCTCTACCTCGACCAGCCGACGGAGATCGCCGCGTACGAACGGGTCTGGAGGGGTCTGGATTCGCT
         >  V  Y  V  E  G  L  T  G  A  L  Y  L  D  Q  P  T  E  I  A  A  Y  E  R  V  W  R  G  L  D  S  L
82870 CGCCCTCGGCGGCGACAATCAGCGGAGCTGGTGATCGATGCCATCCGGGGAGAGTGCTATGAGTGATCTGACCGGCGCCCGCTGGCGCACCAG
         >  A  L  G  A  R  Q  S  A  E  L  I  D  A  I  R  G  E  C  Y  E  •
82961 CACCCCGCAGCGGCACCAACGGCGGGGACTGCGTCGAGGTGGCCGACAACCTCACCGGCATCGTCGGCGTCCGGGACAGCAAGGACCCGGGCG
83053 GGCCGGCCCTGACCGTCCCGCCCGCCGCCTGGTCCGCCTTCGTCACCGAGGTCAAGGCCAACCGCCTCACCCGCTGACAGCTCCGCAACGAA
83145 CCAACCCCCGGCTACGCCTCAGACGCGGCCAGCGCCCCAGGGCTGCCCACGCCTCAGACAGCCCGCGCCTCAGACGTGCCTGCGCCTCAGAC
83237 AGCCCGGGCCGCAGGGGCGCGTGCGCCTCAGACGGCCCGGGCCTCAGAGGGGCGGCGTCGACCGCCTTGCCCAGGGCGGT
                                    <  •  A  R  K  G  L  A  A  D  V  A  K  G  L  A  T
83328 GACGACCAGGGCCACCGAGGGGCGGACCACCGAGTCGTCCAGGCTGACGGTGCCGGAGAAGCCGGCCCCGCCCGGCGATCTCCTCCAGCCGAC
        <  V  V  L  A  V  S  P  R  V  V  S  D  D  L  S  V  T  G  S  F  G  A  G  G  A  I  E  E  L  R  R
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Figure 11V

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83420 GCCGGGCGTCGACGGCGGCGTCGCCGGTCAGGCCGAGCGCCGGCTCCATCCGGAGCACCGCGACCAGGGTGGCCAGCGCCGCCGTCGCCTCG
       < R A D V A A D G T L G L A P E M R L V A V L T A L A A T A E
83512 TCGGGGATCTGCCCGCCGGCCAGCGCCTCGGCCAGCGCCGCCGGGAGTCCTCCTCCACGGTGGCGTCCGCCGTCGGGTAGCGGTGCACGTG
       <D P I Q G G A L A E A L R R R S D E E V T A D A T P Y R H V H
83604 GATGAAGCCCAGCTCGGTCTCCTCGACGTCGCGCACCACGCCCCGGGCGACCAGGTCGCCGAGGATCCGGTCGCGCAGGCCGTGGCGCAGCC
       < I F G L E T E E V D R V V G R A V L D G L I R D R L G H R L R
83696 GCTGCACCCAGGAGGACGGGGTGTGCGGCGTGTCGGCGGCCATCCGGCCCAGGACCTCGTCCAGGATCGGTTCGCCGGTGGGCGCGGGGTCC
       < Q V W S S P T H P T D A A M R G L V E D L I P E G T P A P D
83788 GTGACCACCAGGTTCCCATCGACGTACGCGACCCGGCCGGCGAGGGCCAGCTCGATCAGGACGGCGGCGGCCATCCCGAGGTCGAGGCTGAT
       <T V V L N G D V Y A V R G A L A L E I L V A A A M G L D L S I
83880 CCGCGGCATGGTCGCCTTGCCGGATTCGTCGTCGTACGCGAGGAGCAGCAATTCCTCGGCCAGCGCAACACCAGTCATGGCCGGAGACGG
       < R P M
83970 TAGCGCCTGAGCGCACCCCGTGCGCCCCCAACTCGCCCACGAGCGCACTCGCCCGGTGAGAGGGGAACCCCGCTATACCGCAGGCGTTAACA
84062 GGGGGGCCCTTCCTTGCGATCAGAAGCGGGGCATACCGCCGAACTGGCCGGTCGCCGGCGTCGCCGAGGCCCGGCACGATGAACATCCGGTCG
                    < ° F R P M G G F Q R D G A D G L G P V I F M R D
84153 TTGAGGCTCTCGTCGATCGCGGCGGTGACGAGGCGCAGCGGCAGGCCGGACTGCTCCAGCCGGGCGATGCCGACGGGCGCGGCGAGCACGCA
       <N L S E D I A A T V L R L P L G S Q E L R A I G V P A A L V C
84245 GAGCACGGTGATGTCGGTGCAGCCCGCTCGGCCAGCAGCCGGCAGCAGTGCTCCAGGGAGCCGCCGGTGGCCAGCATCGGGTCGAGGACCA
       < L V T I D T C G R E A L L R C C H E L S G G T A L M P D L V L
84337 GCACGGGCAGGCCGGCGAGGTCGCGCGGCAGCGACTCCATGTACGCGCGCGGCTCGTACGTCTCCTCGTCGCGGGCGAGGCCGACGAAGCCC
       < V P L G A L D R P L S E M Y A R P E Y T E E D R A L G V F G
84429 ATGGACGACTCGGGGAGCAGGGCGAGCGCGGCGTCGGCCATGCCGAGACCGGCCCGCAGCACGGGTACCAGCAGCGGCGGGTTGGCCAGCCG
       <M S S E P L L A L A A D A M G L G A R L V P V L L P P N A L R
84521 GGTGCCCTCGGCGTCGGTGACGGGGGTCTGCACCGGGTACTTCTCGACGGGGAAGGAGCGGGCGGCTTCGTACACGAGCATGGTGGTGAGCT
       < T G E A D T V P T Q V P Y K E V P F S R A A E Y V L M T T L E
84613 CGTGCAGCGCGGCCCGGAAGTTGGAGGAGTCGGTGCGCGCGTCCCGCATGGCGGTCAGCCGCGACTGGGCGAGCGGATGGTCAATGACGTGT
       < H L A A R F N S S D T R A D R M
84705 ACGTCCACGATCGCCCAACCTACCGAACGCCCGGGCCCCGAGCACGAGGAGCGACGCCGCTCACCCGGCCCGTGCGGCAACCCTGGACGGT
84797 TGGCGTTCGAAGGTAGGGCAGGTGCCCAAGGTCGGGCCGACCTCGCCGCGTGATCAAGATCACGAGGCGTGCGGGTGCGTAGACTTCCGGG
84889 CATGACGGCGACAGCGACGTCGGCCCGGTCGGACCTCTCCGAGCTGGACGATCCGAGACCGCTTTGCGGAACTTCCTGCACGGCCTGCCG
       >M T A T A T S A R S D L S E L G R S E T A L R N F L H G L P
84980 GGCGTGGACCAGGTCGGCGCGGAGCAGCGGGCGGCCCAGCTCGGCACCCGCTCGATCAAGACCACGGCCAAGGCCCGGGCGATCGACCTGGC
       > G V D Q V G A E Q R A A Q L G T R S I K T T A K A R A I D L A
85072 GATCCGGATGGTCGACCTGACCACCCTGGAGGGGCGACACCCCCGGCAAGGTGCGGGCGGTCGCGCGCAAAGCACTGCGCCCCGACCCGG
       > I R M V D L T T L E G A D T P G K V R A L A A K A L R P D P
85164 CCGACCCGTCCTGCCCGCACGTCGGCGCAGTCTGCGTCTACCCGGCGATGGTCCCGTACGTGGCCGAGGTGCTGCGCGGATCCGCCGGGTCC
       >A D P S C P H V G A V C V Y P A M V P Y V A E V L R G S A G S
85256 GGGCGGCCGTCCGGCGGACCGGACGGCAACGCGCCGGCCGGACCCGGCGTGGTGCACCTGGCCAGCGTGGCCACCGCGTTTCCGTCCGGGCA
       > G R P S G G P D G N A P A G P V V H L A S V A T A F P S G Q
85348 GGCACCCCTGGAGGTCAAGCTCGCCGACACCCGGGCCGCAGTGGCGGCTGGCGCGGACGAGATCGACATGGTGATCAACCGGGGCGCGTTCC
       > A P L E V K L A D T R A A V A A G A D E I D M V I N R G A F
85440 TGGCCGGCCGCTACCGCGAGGTCTACGACGAGATCGTGGCCACCAAACAGGCGTGCGGGGACGCCCACCTCAAGGTGATCCTGGAAACCGGC
       >L A G R Y R E V Y D E I V A T K Q A C G D A H L K V I L E T G
85532 GAGCTGGCCACGTACGACAACGTGCCGCGGGCGTCCTGGCTGGCCATGCTGGCCGGCGGCGACTTCATCAAGACCTCGACGGGCAAGGTTCC
       > E L A T Y D N V R R A S W L A M L A G G D F I K T S T G K V P
85624 CGTCGCGGCGACCCTCCCGGTGACGCTGGTGATGCTGGAGGCGGTCCGCGACTTCCGCGCCGCCACCGGGCGGCAGGTCGGCGTGAAGCCGG
       > V A A T L P V T L V M L E A V R D F R A A T G R Q V G V K P
85716 CCGGCGGCATCAAGAACACCAAGGACGCGATCAAGTACCTGGTTATGGTCAACGAGACCGTCGGCCCGGACTGGCTGGACCCGGACTGGTTC
       >A G G I K N T K D A I K Y L V M V N E T V G P D W L D P D W F
85808 CGGTTCGGCGCGTCCAGCCTGCTCAACGACCTGCTCATGCAGCGCACCAAGCTGACGACCGGCGTCTACTCCGGTCCCGACTACTTCACCCT
       > R F G A S S L L N D L L M Q R T K L T T G V Y S G P D Y F T L
85900 GGACTGAGCGTGATCTTCGAATACGCGCCCGCCCCCGAGTCCCGCTCGGTGGTGGACCTCAAGCCCTCGTACGGGCTGTTCGTCGACGG
       > D ● > V I F E Y A P A P E S R S V V D L K P S Y G L F V D G
85989 GGAGTTCGTCGACCCGGCCGACGGCGGCGGCTTCAAGTCGGTCAACCCCGCCTCCGAGGAGGTGCTCGCCGAGATCGCCGAGGCGGGCAGCG
       > E F V D P A D G G G F K S V N P A S E E V L A E I A E A G S
86081 CCGACGTGGACCGGGCGGTCCGCGCGCCCGGACGGCGTACGAGAAGGTGTGGGGCCCGATGCCGGGCCGGGACCGGGCCAAGTACCTGTTC
       >A D V D R A V R A A R T A Y E K V W G P M P G R D R A K Y L F
86173 CGGATCGCCCGGATCATCCAGGAGCGCTCCCGCGAGCTGGCCGTGCTGGAGTCCCTGGACAACGGCAAACCGATCCGGGAGTCCCGGGACGT
       > R I A R I I Q E R S R E L A V L E S L D N G K P I R E S R D V
86265 CGACCTGCCGCTGGTCGCCCGCGCACTTCTTCTACTACGCGGGCTGGGCAGACAAGCTGCCGTACGCGGGCTTCGGCCCCGAACCCCCGGCCGC
       > D L P L V A A H F F Y Y A G W A D K L P Y A G F G P N P R P
86357 TCGGCGTGGCCGCGCAGGTCATCCCGTGGAACTTCCCGCTGCTCATGCTCGCCTGGAAGATCGCCCCGGCGCTGGCCGCCGGCAACACGGTG
       >L G V A A Q V I P W N F P L L M L A W K I A P A L A A G N T V
86449 GTGCTCAAGCCGGCGGAGACCACCCCGCTGACCGCGCTGCTGTTCGCCGAGATCTGCCAGCAGGCCGAGCTGCCGGCCGGCGTGGTCAACAT
       > V L K P A E T T P L T A L L F A E I C Q Q A E L P A G V V N I
86541 CGTCACCGGCGCGGGCGACACCGGCGGGCGCTGGTCGAGCACCCGGGCGTGGACAAGGTCGCGTTCACCGGCTCGACCGAGGTCGGCAAGG
       > V T G A G D T G G R L V E H P G V D K V A F T G S T E V G K
86633 CCATCGCCCGGTCCGTCGCGGGCACCGGCAAGAAGGTCACCCTGGAGCTGGGCGGCAAGGCCGCGAACATCGTCTTCGACGACGCCCCGGTC
       >A I A R S V A G T G K K V T L E L G G K A A N I V F D D A P V
86725 GACCAGGCGGTCGAGGGGATCGTCAACGGCATCTTCTTCAACCAGGGGCACGTCTGCTGCGCCGGGTCGCGGCTGCTGGTCCAGGAGTCGGT
       > D Q A V E G I V N G I F F N Q G H V C C A G S R L L V Q E S V
86817 CGCCGAGCAGGTGCTGGAGTCGCTGAAGCGCCGAATGGCGCTGCTGCGGGTCGGCGACCCGTTGGACAAGAACACCGACATCGGGGCGATCA
       > A E Q V L E S L K R R M A L L R V G D P L D K N T D I G A I
86909 ACTCGGCCGCCCAGCTCGCCCGCATCCGCGAGCTGTCCGCCGCGGGCGAGGCCGAGGGGCGGAGCGCTGGTCGCCGCCGTGCGAGCTGCCC
       >N S A A Q L A R I R E L S A A G E A E G A E R W S P P C E L P
87001 GAGCGCGGGTTCTGGTTCGCGCCGACGATCTTCACGGGGGTCACCCAGGCGCACCGGATCGCCCGGGAGGAGATCTTCGGTCCGGTGCTGTC
       >E R G F W F A P T I F T G V T Q A H R I A R E E I F G P V L S
87093 CGTGCTGACCTTCCGCACCCCGGCCGAGGCCGTCGAGAAGGCCAACAACACGCCGTACGGGCTGTCGGCCGGGATCTGGACCGACAAGGGCT
       > V L T F R T P A E A V E K A N N T P Y G L S A G I W T D K G
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Figure 11W

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87185 CCCGGATCCTGTGGATGGCCGACCGGCTGCGCGCCGGGGTGGTGTGGGCCAACACGTTCAACAAGTTCGACCCGACCTCGCCGTTCGGCGGG
      >S  R  I  L  W  M  A  D  R  L  R  A  G  V  V  W  A  N  T  F  N  K  F  D  P  T  S  P  F  G  G
87277 TACAAGGAGTCGGGCTACGGTCGCGAGGGCGGCCGGCACGGGCTGGAGGGGTACCTCGGTGTCTGAGCGGGTCGCGGTACGCAAGACGTAC
      > Y  K  E  S  G  Y  G  R  E  G  G  R  H  G  L  E  G  Y  L  G  V  •
87368 AAGCTCTTCATCGGCGGGAAGTTCCCGCGCAGCGAGTCGGGACGGTCGTATCTCGTGCAATCCGCGAACGTGTCGCTGGCCTCCCGCAAG
                                               > V  Q  S  A  N  V  S  L  A  S  R  K
87458 GACGCGCGGGACGCCGTGGTCGCCGCCCGCGCCGCCGTGAAGGGCTGGGCCGGGGCGACCGCGTACAACCGGGGTCAGATCCTCTACCGGGT
      > D  A  R  D  A  V  V  A  A  R  A  A  V  K  G  W  A  G  A  T  A  Y  N  R  G  Q  I  L  Y  R  V
87550 CGCCGAGATGCTGGAGGGCCGCCGCGAGCAGTTCGTCGCGCTCGGCGTGCCGGCCGACGAGGTCGACGCGGCGATCGACCGCTGGGTCTGGT
      > A  E  M  L  E  G  R  R  E  Q  F  V  A  L  G  V  P  A  D  E  V  D  A  A  I  D  R  W  V
87642 ACGCGGGCTGGTCCGACAAGCTCCCCCAGGTGTACGGCGGTGCGAACCCTGTCGCCGGGCCGTACTTCAACCTGTCCGCGCCCGAGCCGACG
      >Y  A  G  W  S  D  K  L  P  Q  V  Y  G  G  A  N  P  V  A  G  P  Y  F  N  L  S  A  P  E  P  T
87734 GGGGTGGTGGCCGTGGTGGCCCCCGAGGCCCCCGCGCTGCTCGGCCTGGTCAGCGTGATCGCCCCGGCGATCGTCACCGGCAACACGGTGGT
      > G  V  V  A  V  V  A  P  E  A  P  A  L  L  G  L  V  S  V  I  A  P  A  I  V  T  G  N  T  V  V
87826 GGTGGCGGCCTCGCCGACCCAGCCCCTGGCCTCGGTGACCCTGGCCGAGGTGCTGGCCACCTCCGACCTGCCCGGCGGGGTGGTCAACGTCC
      > V  A  A  S  P  T  Q  P  L  A  S  V  T  L  A  E  V  L  A  T  S  D  L  P  G  G  V  V  N  V
87918 TGACCGGTGCGATCACCGAGACGGTGCCGACGCTCGCGGCGCACCTGGACGTCAACGCGATCGACCTGACCGGGGTGGGCGACGCGTCGCTC
      >L  T  G  A  I  T  E  T  V  P  T  L  A  A  H  L  D  V  N  A  I  D  L  T  G  V  G  D  A  S  L
88010 GCCACCGAGCTGGAGGTCAGGGCGGCGGAGAACCTCAAGCGGGTGATTCGGCCGGCCCCGGCCGACCACGACTGGTACGCCGACCCGGGCCT
      > A  T  E  L  E  V  R  A  A  E  N  L  K  R  V  I  R  P  A  P  A  D  H  D  W  Y  A  D  P  G  L
88102 CACCCGGACGACGACGCTGCTGGAGACGAAGACGGTCTGGCACCCCAAGGGCGTCTGAGCCCACCGACCCGTCCACCGACCCGCCCGCCAC
      > T  R  M  T  T  T  L  L  E  T  K  T  V  W  H  P  K  G  V  •
88193 CCGGCCGCCGGAGGCAGGGGTGGGCGGCGGGTGGGGTGGATCTACTACGAGGGGTAGGATTGCCGCGTGACTCGGTTGGGTGATCTTGAGC
88284 GGGCGGTGATGGACGTGCTGTGGGACACCGTCCCGGGCACGTCGGACGGGGTGACGGTGCGCGAGGTCGCCGAGGCCCTCGACGGCCGCGA
                  > M  D  V  L  W  D  T  V  P  G  T  S  D  G  V  T  V  R  E  V  A  E  A  L  D  G  R  E
88375 GCTGGCGTACACGACGGTGATGACCGTGCTGGACCGGCTCGCCGGCAAGGGCATGGTGCGGCGCCAGCGGGAGGGGCGGGCCTGGCGCTACC
      > L  A  Y  T  T  V  M  T  V  L  D  R  L  A  G  K  G  M  V  R  R  Q  R  E  G  R  A  W  R  Y
88467 AGGCCGCGGCCAGCCGCGAGGCGCACATCGCCCAGCTCATGCTCGACGCGGACCTCGGCGGCAGCCGGGACGCCGCGCTGGTGCGCTTC
      >Q  A  A  A  S  R  E  A  H  I  A  Q  L  M  L  D  A  L  D  L  G  G  S  R  D  A  A  L  V  R  F
88559 GCCCGGTCGGTGACCGGCACCGAGGCCGAGGTGCTGCGCGCCGCCCTCGGCGCCGAGGCGGGCGGCCCGCTGACCGACCGCGTCGACGCGCC
      > A  R  S  V  T  G  T  E  A  E  V  L  R  A  A  L  G  A  E  A  G  G  P  L  T  D  R  V  D  A  P
88651 GCGCGCCGACCGGGCCGGCCAGCCCGGCCCTGGCCGACGAGGCGACGGACCGGTAGGGCCGCCGTCATGGCGTACGCCGTGCACTTCGCCG
      > R  A  D  R  A  G  Q  P  A  L  A  D  E  A  T  D  R  •       > M  A  Y  A  V  H  F  A
88741 CGACGGTCCTGGCCTGCTACCTGACCGCTCAGGTCCTGGCGGCGTCCACCTGGACGTGGCGGGGCCCCCCGGATCGCGATCGTCTGCTGGCAG
      >A  T  V  L  A  C  Y  L  T  A  Q  V  L  A  A  S  T  W  T  W  R  A  P  R  I  A  I  V  C  W  Q
88833 GCGGTCGGGCTCGCGCTCGGGCTCTCCGCGATGGGCCTGCCGATGGCGCTCGGCGTGGCCGCGTACGACCGGCCGACCGGCAGCGCGTTGCT
      > A  V  G  L  A  L  G  L  S  A  M  G  L  P  M  A  L  G  V  A  A  Y  D  R  P  T  G  S  A  L  L
88925 CGCCCTGGCCACCGACCTGACCCACGGCACCCTGCCCGGCCCGGGCTCGGCGGCGGTCCACCTCGGTCTGGTCGGGGGTCGGGTTCGGCATCGGGG
      > A  L  A  T  D  L  T  H  G  T  L  P  A  G  L  G  A  V  H  L  G  L  V  G  V  G  F  G  I  G
89017 CGGCGCTGCTCGCCACGACGGTACGCAGCGTGCAGGCGACCGTCCGGGCCCAGCGGCAGCACCGGGACCTGCTCGCCCTGGTGGCCCGGCGG
      >A  A  L  L  A  T  T  V  R  S  V  Q  A  T  V  R  A  Q  R  Q  H  R  D  L  L  A  L  V  A  R  R
89109 GACCCGGAGGTGCCGGGGGCGCTGGTGCTGGACCATCCGAGCGCGGCGGCGTACTGCCTGCCGGGCGTGCGGCCCCGGGTGGTGGTCAGCGC
      > D  P  E  V  P  G  A  L  V  L  D  H  P  S  A  A  A  Y  C  L  P  G  V  R  P  R  V  V  S  A
89201 CGGGGCGCTCAGCATGCTCGACCGGGCCGAGCTGGCGGCGGTGCTGACCCACGAGCGGGCGCACGCCCAGGAGCGCGCCCACGACCTTGTGCTGC
      > G  A  L  S  M  L  D  R  A  E  L  A  A  V  L  T  H  E  R  A  H  A  Q  E  R  H  D  L  V  L
89293 TGCCGTTCACCGCGCTGTGCCGTGCGCTGCCCTGGTTCCGTTGGGTACGCGACGCGCACGAGCGGGTCGCCCTGCTGGTCGAGATGCGCGCC
      >L  P  F  T  A  L  C  R  A  L  P  W  F  R  W  V  R  D  A  H  E  R  V  A  L  L  V  E  M  R  A
89385 GACGACAAGGCCCGGGAGCTGCACGCCGAGGCTCCCCTCGCGGGGGCGTTGCGCCGGTTCGCCGCGGCCGGCCACCGGATCGCGCCGGCCGG
      > D  D  K  A  R  E  L  H  A  E  A  P  L  A  G  A  L  R  R  F  A  A  A  G  H  R  I  A  P  A  G
89477 CACCCTCGGCCTGGGCGACCGGGACCTGGACGTCCGGGTCCAGCGGCTGCTGGTCGCCGACCGGCCGCCCCGGCTGATCGGGGCCGCCGCGC
      > T  L  G  L  G  D  R  D  L  D  V  R  V  Q  R  L  L  V  A  D  R  P  P  R  L  I  G  A  A
89569 TGGCGGTGGCGGTCACCCTGGTCGCGCTGCCGGTCTCCCTCTTCCTGAGCTGACGCCCGACCCGGACACGTCCGACCCGGACACGCGCGAC
      >L  A  V  A  V  T  L  V  A  L  P  V  S  L  F  L  S  •
89661 CGGACACGTCCGACCCGGACGCCTCGCCCGAGTTGGGCCCGTGTCCCACGGGCCGGGCTCGCCTGCCCGTTGCCGGGCCACCGACATGCGGG
89752 GCGATAGGTAGAGAGCCTACGTGTAGTCTTCCTACGACAAGGGAGCCTACTACCGGAGGGCGGCCATGGATCAACTGCTCCTCGCCCGTC
                                                                   > M  D  Q  L  L  L  A  R
89842 TCCAGTTCGCCACGACCACCTCGCTGCACTTCCTCTTCGTCGTCGTCACGCTCGGTCTGGTCACCCTGCTCGTCGGGCTCCAGACGGCCTGG
      >L  Q  F  A  T  T  T  S  L  H  F  L  F  V  V  V  T  L  G  L  V  T  L  L  V  G  L  Q  T  A  W
89934 ACGATCACCGGCAATCCCGTCCACGAGCGGCTGACCCGGTTCTGGGGTCAGCTCTACGTGATCAACTACGTGCTCGGCATCGCCACCGGCCT
      > T  I  T  G  N  P  V  H  E  R  L  T  R  F  W  G  Q  L  Y  V  I  N  Y  V  L  G  I  A  T  G  L
90026 GCTCATGGAGTTCCAGTTCGGGCTGAACTGGAGCGGCCTGTCGCGCTACGTCGGCAACGTCTTCGGCGCCCCGCTGGCGATCGAGACCCTGG
      > L  M  E  F  Q  F  G  L  N  W  S  G  L  S  R  Y  V  G  N  V  F  G  A  P  L  A  I  E  T  L
90118 TCGCGTTCTTCCTGGAGTCCACGTTCCTCGGGATGTGGATCTTCGGCTGGCACCGGCTGCGCCGGGGCGTGCACCTCGCGCTGCTGTGGGGC
      >V  A  F  F  L  E  S  T  F  L  G  M  W  I  F  G  W  H  R  L  R  R  G  V  H  L  A  L  L  W  G
90210 GTGGCGCTGACCGCGTACGCCTCGGCGTTCTGGGTCATGGTGGCGAACGCCTGGCTGCAGAACCCGGTCGGCTACGAGGTGCGCGACGGGGT
      > V  A  L  T  A  Y  A  S  A  F  W  V  M  V  A  N  A  W  L  Q  N  P  V  G  Y  E  V  R  D  G  V
90302 GGCCCACCTGACCGACTTCGGCGCGTTGCTGACCAATCCCACCTTCGGCCTGGCCTTCGGGCACGTGGTCGCCGCCGCCCTGCTCACCGGCG
      > A  H  L  T  D  F  G  A  L  L  T  N  P  T  F  G  L  A  F  G  H  V  V  A  A  A  L  L  T  G
90394 GGATGCTGATGGCGGCGGTGAGCGCCTGGCACCTGATCCGGCGCACCCCGGACCACGCGCTGTTCCGCACGTCGCTGCGGATCGGCCTGGTC
      >G  M  L  M  A  A  V  S  A  W  H  L  I  R  R  T  P  D  H  A  L  F  R  T  S  L  R  I  G  L  V
90486 ACCGCGGCGGTCTCGATCAGCCTGGTGCAGGGCTTCGGCTTCGCCCAGTTCGGGCCGGTCGGGCAGCGGCAGCCCCACCAAGTTCGGCGGCGG
      > T  A  A  V  S  I  S  L  V  Q  G  F  G  F  A  Q  F  G  G  P  V  G  Q  T  Q  P  P  T  K  F  G  G  G
90578 CGCGCAGCGCGACGCCCTGGTCGCCGAATGGACCTCCCGGTTCGGGCCCGGCGACTACACCCCGCCCGTGCTGGCCGACGTCGGGCTCGGTT
      > A  Q  R  D  A  L  V  A  E  W  T  S  R  F  G  P  G  D  Y  T  P  P  V  L  A  D  V  G  L  G
90670 TCATGATCCTGATCGGCCTCCTCCTGGGCTGTCTCGTGGCTGCTGCTCCCCCTGCTCTGGCGGGACTGGTTCATCCGGCTGCGCTTCCCGCTC
      >F  M  I  L  I  G  L  L  L  G  C  L  W  L  L  L  P  L  L  W  R  D  W  F  I  R  L  R  F  P  L
90762 TGGCTGATCCTGCTGGCGCTGCCGCTGCCCTTCGTCGCGGTGATCCTCGGCTGGATCGCCCGTGAGGTGGGCCGCCAGCCCTGGGTCGCGTA
      > W  L  I  L  L  A  L  P  L  P  F  V  A  V  I  L  G  W  I  A  R  E  V  G  R  Q  P  W  V  A  Y
```

Figure 11X

```
90854 CGGGCTGCTTTCCACCGAGCGGGCGGTCTCGCCGGTCGCGCCCGGGGTGATGCTCGCCTCGCTGATCGGCTTCACCCTGCTGCTCGGCGGGC
       > G  L  L  S  T  E  R  A  V  S  P  V  A  P  G  V  M  L  A  S  L  I  G  F  T  L  L  L  G  G
90946 TCGCCGTCGCCAACTGGGTGCTGTTCGCCCGGTACGCCGCCCGGGGAGCCGCCGATCCCGCCCTAGGCCGCCGGCCCGGCCCAGCCGCCGAC
       >L  A  V  A  N  W  V  L  F  A  R  Y  A  A  R  G  A  A  D  P  A  L  G  R  R  R  P  G  P  A  A  D
91038 GAGTCCCGTCCCGTCCCCGTCCTCGGCTGAGGAGGCCCCTGTGGAACTCGCCTGGTACGCCCTGCTCGGGCTCTTCCTCGCCGGCTACC
       > E  S  R  P  V  P  V  L  G  °       > V  E  L  A  W  Y  A  L  L  G  L  F  L  A  G  Y
91127 TGGTCCTCGGCGGCTACGACTACGGCGTCGGCCTGCTGCTCGCCCGGGGCGGCCCGCCGGCCCGCCGCCGGGCGGCCCTCACCGCCGTGGGC
       >L  V  L  G  G  Y  D  Y  G  V  G  L  L  L  A  R  G  G  P  P  A  R  R  R  A  A  L  T  A  V  G
91219 CCGTTCTTCCTCGGCAACGAGGTCTGGCTGGTGGCGACCGTCGGCATTCTGTTCGGCGCGTTCCCCACCCTGGAGGGGGAACTGCTGTCCGG
       > P  F  F  L  G  N  E  V  W  L  V  A  T  V  G  I  L  F  G  A  F  P  T  L  E  G  E  L  L  S  G
91311 CTTCTACCCCGTCGTCGCCGCCGCGCTGGCCGGGGTGATCATGGTGACCGTCGGCGTGCAACTGCGCAGCCGCCCGACCGACGAGCCGACCC
       > F  Y  P  V  V  A  A  A  L  A  G  V  I  M  V  T  V  G  V  Q  L  R  S  R  P  T  D  E  P  T
91403 GCGCCGCCTGGGACCGGATGGTGGCCGCCGGGAGCCTGCTCGCCGCGTTCGGCTGGGGGGCGCTGCTCGCCGGGCTGCTCCAGGGCGTACCG
       >R  A  A  W  D  R  M  V  A  A  G  S  L  L  A  A  F  G  W  G  A  L  L  A  G  L  L  Q  G  V  P
91495 CTGGCCGCCGACGGGCACGTCACGGGCGTCGGCCACGTGGCCACCCCGTTCGCGGCCCTCGCCGGGCTGGCGATGACGGCCCTGGTGGCGGT
       > L  A  A  D  G  H  V  T  G  V  G  H  V  A  T  P  F  A  A  L  A  G  L  A  M  T  A  L  V  A  V
91587 GCACGGTGCGACGTTCCTCACGCTCCGGCTGTCGGCCGCCGACGCCGCACCGCTGGCCCGTACCGCCCGGCTGGTCGCGGTGGCGCTCG
       > H  G  A  T  F  L  T  L  R  L  S  A  A  D  A  A  P  L  A  R  T  A  R  R  L  V  A  V  A  L
91679 CCGCCGTCGCCCTGGCCGCCGTCGCGGGCGCGCTCTCCGATCGGGTACGCGCCGCGACGCAGCGCCCGCTGCCGGCCGTACTGCTGCCGTTG
       >A  A  V  A  L  A  A  V  A  G  A  L  S  D  R  V  R  A  A  T  Q  R  P  L  P  A  V  L  L  P  L
91771 GTACTGGTGGCGGCGCTGCTGGTGGCCCGGGCGGCGCACGGCGCACCTGCCCGGGGTGGCCTTCGCCGCCACTTCGGCGGCGCTGGCGCT
       > V  L  V  A  L  L  V  A  R  A  A  H  A  R  H  L  P  G  V  A  F  A  A  T  S  A  A  L  A  L
91863 GCCGGTGGCGGGAGTCGGCGCGGCGTTGTGGCCCTACGCGCTGGTCTCCACCGTCGCCACCGACGGCATCACTGAGCGTGACCGACGCGGCGG
       > P  V  A  G  V  G  A  A  L  W  P  Y  A  L  V  S  T  V  A  P  T  A  S  L  S  V  T  D  A  A
91955 CCAGCGGGCCGACGCTGACGGTGCTGGGCTGGCTGGCGCTACCGCTCCTGCCGGCCCTACTAGGCTTCCAGGCGATGTGCTGGTGGGTGTTC
       >A  S  G  P  T  L  T  V  L  G  W  L  A  L  P  L  L  P  A  L  L  G  F  Q  A  M  C  W  W  V  F
92047 CGGGGACGAACCGACGGCAGGGCACCGGTGTACTGGTGAGCCGCCGTCCCTTCGACCCACGTCTGCTCCGCCGGGTCCCCGCGGCCCGGCG
       > R  G  R  T  D  G  R  A  P  V  Y  W  °
92138 CGACCTCGCCGTGCTCGCGGTGCTCGGCGGGCTGACGGCGCTGCTGGTCGTGGGGCAGGCCACCGCGCTGGCCACGGTGCTGGCCGCCGCG
       > V  L  A  V  L  G  G  L  T  A  L  L  V  V  G  Q  A  T  A  L  A  T  V  L  A  A  A
92229 CTCGACGGGCGGTTGGCCCGGCCGGCGCTCGCCGGTTTCCTGGCCGCCGTGGTGGGGCGGGCGCTGGTCGCCTGGGCCCAGGGCACGGTGGC
       >L  D  G  R  L  A  R  P  A  L  A  G  F  L  A  A  V  V  G  R  A  L  V  A  W  A  Q  G  T  V  A
92321 GGCGCGGGCCGCCGCGACGGTCAAGGCGGCGCTGCGGGCCGACCTCGCCGCCGTCGGCCGGCACGGTCCCGGCTGGGTCGCCGGGCAGC
       > A  R  A  A  A  T  V  K  A  A  L  R  A  D  L  L  A  A  V  G  R  H  G  P  G  W  V  A  G  Q
92413 GGGCCGGGCAGCTCGCCACCCTGGCCGGGCGGGGGCTGGACGCCCTGGACGCCTACTTCACCGGGTACCTTCCGCAGCTCGTGCTCAGCGTC
       >R  A  G  Q  L  A  T  L  A  G  R  G  L  D  A  L.D  A  Y  F  T  G  Y  L  P  Q  L  V  L  S  V
92505 ACCGTCCCGGTGGCCGTGCTGGCCCGGATCACCTTCGCCGACTGGGGCTCGGCCGTCATCGTCGCGCTGACCCTGCCGCTGATCCCGGTCTT
       > T  V  P  V  A  V  L  A  R  I  T  F  A  D  W  G  S  A  V  I  V  A  L  T  L  P  L  I  P  V  F
92597 CGGGGGCGCTGCTCGGCTGGCAGGCGCAGGCCGCCACCGAGCGGCAGTGGCGGCGGCTGTCGACGCTCGGCGGGCACTTCCTCGACATGGTCG
       > G  A  L  L  G  W  Q  A  Q  A  A  T  E  R  Q  W  R  R  L  S  T  L  G  G  H  F  L  D  M  V
92689 CCGGCCTGCCCACGCTGCGCGCGTTCGGCCGGGCCCGGGGCCAGGTCGAGGTGGTCCGCCGGATGGCCGACGGGCACCGCGCCGCGACGATG
       >A  G  L  P  T  L  R  A  F  G  R  A  R  G  Q  V  E  V  V  R  R  M  A  D  G  H  R  A  A  T  M
92781 CGCACGCTGCGGATCGCGTTCCTGTCCGCGCTGGTGCTGGAGCTGGTCGCCACCCTGTCGGTGGCGCTGGTCGCGGTGCCGGTGGGCATCCG
       > R  T  L  R  I  A  F  L  S  A  L  V  L  E  L  V  A  T  L  S  V  A  L  V  A  V  P  V  G  I  R
92873 GCTGCTCGGCGGCGGGCTGGCGCTGTCCACCGCGCTGCTGGTGCTGCTGCTCACCCCGGAGGCGTACCTGCCGCTGCGGGCGGCCGGCAGCC
       > L  L  G  G  G  L  A  L  S  T  A  L  L  V  L  L  L  T  P  E  A  Y  L  P  L  R  A  A  G  S
92965 GGTTCCACGCCAGCATGGAGGGGCTGGCCGCGCTGGACGAGGCACTGACCCTCTCCGCCGCCGACCCGACCGCCACGGCCACCGCCGGGTCG
       >R  F  H  A  S  M  E  G  L  A  A  L  D  E  A  L  T  L  S  A  A  D  P  T  A  T  A  T  A  G  S
93057 CGGCCCGTCCCCGACGGGCGCGCCGAGATCCGGTTCGAGGGCGTGACCGTCGCGTACGAGCGGACGGTGGCCGTACGGGACGTCACGCTGAC
       >R  P  V  P  D  G  R  A  E  I  R  F  E  G  V  T  V  A  Y  E  R  T  V  A  L  R  D  V  T  L  T
93149 AATCCGGCCCGGCGAGCGGATCGCGATCGTCGGGCCGAGCGGCGCGGGCAAGAGCACCCTGCTCAACCTGCTGCTCGGCTTCGTCGCCCCGA
       > I  R  P  G  E  R  I  A  I  V  G  P  S  G  A  G  K  S  T  L  L  N  L  L  L  G  F  V  A  P
93241 CGCAGGGCCGGGTCACCGTGGGTGGCGTCGACCTGGCCGGCGCGGACCCGGACGGCTGGCGGCGTCAGGTCGCCCTGGGTGCCGCAACGGGCC
       >T  Q  G  R  V  T  V  G  G  V  D  L  A  G  A  D  P  D  G  W  R  R  Q  V  A  W  V  P  Q  R  A
93333 CACCTCTTCGCCGCCTCGCTGACCGACAACATCCGGCTCGGTGCCCCCGGCACGCCCGACGCCGCGCTCGCCGGCGCGGTCGCCGCCGCCGC
       >H  L  F  A  A  S  L  T  D  N  I  R  L  G  A  P  G  T  P  D  A  A  L  A  G  A  V  A  A  A  A
93425 GCTGGACGAGGTGGTCGCCGCCCTGCCCGACGGGCTCGACACCGTGCTCGGTGAGCGCGGGCACGGCCTGTCCAGCGGCCAGCGGCAGCGGG
       > L  D  E  V  V  A  A  L  P  D  G  L  D  T  V  L  G  E  R  G  H  G  L  S  S  G  Q  R  Q  R
93517 TCGCCCTGGCCCGGGCGTTCCTGCGGGACGCGCCGGTGGTGCTGCTGGACGAGCGCGACCGCGCGGCGTGGACACCGCCAGCGAGGCCGGGGTG
       >V  A  L  A  R  A  F  L  R  D  A  P  V  V  L  L  D  E  P  T  A  R  L  D  T  A  S  E  A  G  V
93609 CTGGCCGCCACCCGCCGGCTCGTCGCCCGGGCGAACCGCCCTGTTGGTGGCCCACCGGCCGGCGCTGCTCTCCGACGCCGACCGGATCCTGCG
       > L  A  A  T  R  R  L  V  A  G  R  T  A  L  L  V  A  H  R  P  A  L  L  S  D  A  D  R  I  L  R
93701 GGTCGAGGAAGGCCGGGTCACCGAGCTGACCACCACCCCGGCCACAGGGGTGACCCCCGGCCCCGGCGAGGCGGCTGCCGGACCGGCCGGGC
       > V  E  E  G  R  V  T  E  L  T  T  T  P  A  T  G  V  T  P  G  P  G  E  A  A  A  G  P  A  G
93793 AGGTCGCCCCCGCCCCGGCCGGAGAGGGGGCGGCCCGATGAGCACCGGTCCCGCCGACGACGCCTTCGCCATCCCGCTGCCGGCCGACGGG
       >Q  V  A  P  A  P  A  G  E  G  A  A  R  °
                                                  > M  S  T  G  P  A  D  D  A  F  A  I  P  L  P  A  D  G
93884 GCCCCGGTGGCCGGCGGCAGCGTCCGGGCCGCCGAGCGGGCCGTGCTCCGGCTGGCCCGGCCGTACCTGGGCCGGCTGGTCGGCGCGGGTCT
       > A  P  V  A  G  G  S  V  R  A  A  E  R  A  V  L  R  L  A  R  P  Y  L  G  R  L  V  G  A  G  L
93976 GCTCGCCGCCGCCACCGAGTTCGCCGGCCTGGCCCTGATGGCCACCGCCACCTGGCTGCTGATGAGCGCCGCCGGTCGGCCACCACTGGACC
       > L  A  A  A  T  E  F  A  G  L  A  L  M  A  T  A  T  W  L  L  M  S  A  A  G  R  P  P  L  D
94068 GGCTCACCGTGGCGATCGTCGCGGTCCGGGCGCTGGCGATCAGCCGAGGCGTGTTCCGCTACACCGAGCGCCTCGCCGGCCACGATGCCGTG
       >R  L  T  V  A  I  V  A  V  R  A  L  A  I  S  R  G  V  F  R  Y  T  E  R  L  A  G  H  D  A  V
94160 CTGCGGATGATCACCGACGTCCGGGCCGGGGTCTTCGCCGCCCTGGCCGCCCGGCGCGACGCCGCCCGGCAGCGCACCGGGGACGCGCTGAG
       > L  R  M  I  T  D  V  R  A  G  V  F  A  A  L  A  A  R  R  D  A  A  R  Q  R  T  G  D  A  L  S
94252 CCGGCTCGTGTCCGACGTGGAGGCCGTGCAGGACCTGCTGCTGCGGGTGCTCGTCCCGGGGGCCGCCGCCACGGTGGTCAGCGTGCTGGCCG
       > R  L  V  S  D  V  E  A  V  Q  D  L  L  L  L  R  V  L  V  P  G  A  A  A  T  V  V  S  V  L  A
94344 TGGCCGGGGCCACCACCATCTCGCTCCCCGCCGCCGGGGTGCTGGCGCTGGGCCTGCTCGTCGCCGGGGTGGCCCTGCCGCTCGCGGCCACC
       >V  A  G  A  T  T  I  S  L  P  A  A  G  V  L  A  L  G  L  L  V  A  G  V  A  L  P  L  A  A  T
```

Figure 11Y

```
94436 GCGCTGACCCGGCACGCCGCCGACCGGGTGGCCCCGCTGCGCGGCGCGCTCGCCACGGACGCCGTGGACCTTGTCCACGGCGCCGCCGACCT
         >  A  L  T  R  H  A  A  D  R  V  A  P  L  R  G  A  L  A  T  D  A  V  D  L  V  H  G  A  A  D  L
94528 GGCCGCGTTCGGTGCCACCGGGTACGCGCTGGACGCCGCCGCCGATCGGGCCCGCCGGCTGGCCCGGCTGGAACGACGGCTCGCCGCCACCG
         >  A  A  F  G  A  T  G  Y  A  L  D  A  A  A  D  R  A  R  R  L  A  R  L  E  R  R  R  L  A  A  T
94620 GCTTCGCCGTGGACGCCGCCGGGGCGCTCGTCGCCGGGGTGACCGCCGGCACGGTGGTGGTCACCGCGCTGCGCGACGGCGTCGGCGGGGTG
         >G  F  A  V  D  A  A  G  A  L  V  A  G  V  T  A  G  T  V  V  V  T  A  L  R  D  G  V  G  G  V
94712 CTGGTCGGGGTGCTGGCGGTCGGTTCCCTGGCCGCCGTCGAGGTGGCGCTGGCGCTGGTCGGGGCGCGCCCGGCAGCGCACCCAGCTCCGGGC
         >  L  V  G  V  L  A  V  G  S  L  A  A  V  E  V  A  L  A  L  V  G  A  A  R  Q  R  T  Q  L  R  A
94804 CGGGCTGGTCCGGGTGGCCGCCCTGCTGACCGCCCCGCAGGCCGACGCGCCCGCCGCCACCCCGCCCGGTGCCGCCCGTGCCGCCGCCGTCG
         >  G  L  V  R  V  A  A  L  L  T  A  P  Q  A  D  A  P  A  A  T  P  P  G  A  A  R  A  A  A  V
94896 GTGCCGGGCCCGCACGACGTGCGCTTCGACGCGGTCACCGTGCGGTACCGGGCCGGCACCGCCCCGGCCCTGGACCGGGTCACCCTGGACCTG
         >G  A  G  P  H  D  V  R  F  D  A  V  T  V  R  Y  R  A  G  T  A  P  A  L  D  R  V  T  L  D  L
94988 CCGGCCGGCCGCCGGGTCGCCGTGGTCGGGCCGAGCGGCGCCGGCAAGAGCACCCTCGCCGCCGTCCTCACCGGCACGGTGCGACCCGAGCA
         >  P  A  G  R  R  V  A  V  V  G  P  S  G  A  G  K  S  T  L  A  A  V  L  T  G  T  V  R  P  E  Q
95080 GGGCCGGGTCACCCTCGACGGGGCCGACCTGTCGGCGTACCGGTCGAGGAACTGCCCCGGGCCGTCGGCGGCCTGCTCGCCGAGGCGTACG
         >  G  R  V  T  L  D  G  A  D  L  S  A  Y  P  V  E  E  L  P  R  A  V  G  G  L  L  A  E  A  Y
95172 TCTTCCACGCCACGGTCCGGGAGAACCTGCTGCTCGGCCGGCCCGCCGCCGACGAGGCGGAGCTGACCGCCGCGACCCGGGCGGCCGGCCTG
         >V  F  H  A  T  V  R  E  N  L  L  L  G  R  P  A  A  D  E  A  E  L  T  A  A  T  R  A  A  G  L
95264 CTGGACTGGGTGCACGCCCAGCCGGCCGGGTGGGACACCGTGGTCGGCGAGGAGGGCGGACAGCTCTCCGGCGGCCAGCGGCAGCGCCTCGC
         >  L  D  W  V  H  A  Q  P  A  G  W  D  T  V  V  G  E  E  G  G  Q  L  S  G  G  Q  R  Q  R  L  A
95356 GCTGGCCCGGGCGCTGCTCGCCGCGCCCGGGGTGCTGGTGCTCGACGAGCCGACCGAGGGGCTCGACCCGTCCGCCGCCGACGCGGTGCTCG
         >  L  A  R  A  L  L  A  A  P  G  V  L  V  L  D  E  P  T  E  G  L  D  P  S  A  A  D  A  V  L
95448 CCTCGGCGCTGGCGGCGACCCCCGCCGGGCACTCGGTGCTGCTGATCAGCCACCGGCTCAGCGGGCTCGCCGACCTCGACGAGATCGTGGTG
         >A  S  A  L  A  A  T  P  A  G  H  S  V  L  L  I  S  H  R  L  S  G  L  A  D  L  D  E  I  V  V
95540 CTCGACGCCGGCCGGGTGGTCCAGCGTGGCCGGCACGACGAGTTGGTCGCCGCGCCCGGGCTGGTACCGGGACCAGTGGCTGCTCCAGGAGGC
         >  L  D  A  G  R  V  V  Q  R  G  R  H  D  E  L  V  A  A  P  G  W  Y  R  D  Q  W  L  L  Q  E  A
95632 GGCCGAGCGGGTACCTGGCCCTGACGCCGCCCCTGAGCCGGCTCCGGGATTCCCCCGGACGCGTCGGCAGTCACCGCATGGCAGGCT
         >  A  E  R  G  Y  L  A  L  T  P  R  P  •
95723       CGTCGCATGGTGCGCTGCGACGACGTACTCGTGAAGGAGCGGCTGCGCGAGTTGAGCGACCGGCTGCACGGCCCGGCACGGCTCAAGGCCG
                >  M  V  R  C  D  D  V  L  V  K  E  R  L  R  E  L  S  D  R  L  H  G  P  A  R  L  K  A
95814 ACCTGCTGGCCGAGGCCCGCCACGCGTTGCAGGACGCCGTCGAGGCGTACCGGGACGGCGGGCTGCCGGCGGCGGAGGCCGAGCGGCGGGCA
         >D  L  L  A  E  A  R  H  A  L  Q  D  A  V  E  A  Y  R  D  G  G  L  P  A  A  E  A  E  R  R  A
95906 GTGGCCGAGTTCGGCGAGCCGGCCCGGCTCGCCCCGGCGTACCAGGCGGACTGGCGGCCCGGGTCGCTGCGGCTGTCCCTGCGGGTGCT
         >  V  A  E  F  G  E  P  A  R  L  A  P  A  Y  Q  A  E  L  A  A  G  S  L  R  G  L  S  L  R  V  L
95998 CGCGGTCGCCGGCGTCCTGGTCGTCGCGGGCGATCTGACCTGGCAGGGGTCGAGCTGGAGCGGCGGCCCCGGCCCGCCGGCGGCCTACCGCC
         >  A  V  A  G  V  L  V  V  A  G  D  L  T  W  Q  .G  S  S  W  S  G  G  P  G  P  P  A  A  Y  R
96090 TGCTGTCCGCCTCGGTGGACGGCATCTGGCTGGGCGCGGTCGTGCTGTCGGTGGCGGGGTTGCTGCTGGTCGCCGCCTCGGCCCGGTGGGCG
         >L  L  S  A  S  V  D  G  I  W  L  G  A  V  V  L  S  V  A  G  L  L  L  V  A  A  S  A  R  W  A
96182 CACCCGGCCCTGCCCCGGCTCGCCCGGCTGACCGGTCTCGGGCTCACCGCCACGCTCGTCCTGGGCGTGGACCGGCGCGGCCCTGTACGC
         >  H  P  A  L  P  R  L  A  R  L  T  G  L  G  L  T  A  T  L  V  L  G  V  A  T  G  A  A  L  Y  A
96274 CTGGTCGATCGGGCTCTGGGAGGCGGCCCGCACCTGGCCGCCGATGCTCGTGGGCGCGCTGGTCTGCGGCGCGGGGTTCTTCTGGATCGGTC
         >  W  S  I  G  L  W  E  A  A  R  T  W  P  P  M  L  V  G  A  L  V  C  G  A  G  F  F  W  I  G
                                                                             junction marker
96366 GGGCGGCCCGGTCCTGGCTGCTCTCGGCACGCCGACCGGCCGGACCGGCGTAGTCGGGTGGCGGCGGGGCGCGGTCAGGCCGGCGGTGGCGG
         >R  A  A  R  S  W  L  L  S  A  R  R  P  A  G  P  A  •                    <  •  A  P  T  A  P
96457 GGGTGTCGCCGAGGAACTGGCCGACGGTCGCGCTGAACTCCCGCCAGCCGGCCCGTTCCCCGGCGAGGGCCCGGCCGGAGTCGGTCAGC
          <  T  D  G  L  F  Q  G  V  T  A  S  F  E  R  W  G  A  R  E  G  A  L  A  R  R  G  S  D  T  L
96549 TCGTAGGTCGGCGCTCGCGGCCGTTGACGGTGCTCCAACTGCTGACCACGTGCCCCGCCCGCTCCAGCCGGCGCAGCGCCGGGTAGATCGT
         <E  Y  T  R  R  E  R  G  N  V  T  S  W  S  S  V  V  H  G  A  R  E  L  R  R  L  A  P  Y  I  T
96641 CCCGGTAGGCAGATCGAGGCTGCCCTCGCTGCGCGCGCAGCGCCTCGATGATGGCGTAGCCGTGCAGCGCGCCCCGTTCCAGCACCGCGA
         <  G  T  P  L  D  L  S  G  E  S  R  A  R  L  A  E  I  I  A  Y  G  H  L  A  G  R  E  L  V  A  L
96733 GCAGCAGCGCGTCGAGGTGTCCGTGCAGCGCCTGGGCCTTCATAGGTAGCAAGACTACTTGTGGGCCACTCGCCGCCGCCACCGGGGTGCGG
         <  L  L  A  D  L  H  G  H  L  A  Q  A  K  M
96824 GCACCGGGCCTCCTAAGCCGCCCACTAGGGTATGTGCCCAGAGTCACTCGGCGGCCGGAGACGCCGCCGGGTGGGCAGCCCGAAGCACAC
                                                              >  V  G  S  P  K  H  T
96914 GGAGGTCAGCGTGGCCCGCCAGTCGCCCCAACGGCCCGACGCCGACGAGCCTGAGCTCGACGAGACCGACGGCACCGCCGCAGAGGTCGAAG
         >  E  V  S  V  A  R  Q  S  P  Q  R  P  D  A  D  E  P  E  L  D  E  T  D  G  T  A  A  E  V  E
97006 AGGACGGCGCGCGCCCGTCGGCGCAGGACGCCGACCGCGCGCTCTGGGACGAGCTGCGCATCGACCCGGTCGAGATCGCCCTGCCCGCCGGC
         >E  D  G  A  R  P  S  A  Q  D  A  D  R  A  L  W  D  E  L  R  I  D  P  V  E  I  A  L  P  A  G
97098 ACCGGCTACACGCTGCGGGCGTACCGGCCGGCACGGGAGTTGACCCCGACCGACGTCGCCGAGCGCGACCAGGACGACCCGTTCCTGGCCCG
         >  T  G  Y  T  L  R  A  Y  R  P  A  R  E  L  T  P  T  D  V  A  E  R  D  Q  D  D  P  F  L  A  R
97190 CCGGCAGGCGGTCGAGACCGACGAGGACGAGGACGAGGTCATCATCCTCGACGAGGAGGTGGCCGCCGAGTTCGCCGAGGCGGACGCGGAGG
         >  R  Q  A  V  E  T  D  E  D  E  D  E  V  I  I  L  D  E  E  V  A  A  E  F  A  E  A  D  A  E
97282 AGGCCGGCGGGAAGTCCCGCTCCCGCAAGCCCCGCGCCGACGCGGACTCCGACGACGCCGGAGCCGCCACAGACGCGGACGCGGAGGAGGAG
         >E  A  G  G  K  S  R  S  R  K  P  R  A  D  A  D  S  D  D  A  G  A  A  T  D  A  D  A  E  E  E
97374 CCGGACTCCGACGAGGACGAGGCGGGCGACGAGGAGGTTCCGGTCTTCCTCAGCCACCGGGGCAGGCTGCTGCTGTTCAAGACGCCCGAATC
         >  P  D  S  D  E  D  E  A  G  D  E  E  V  P  V  F  L  S  H  R  G  R  L  L  L  F  K  T  P  E  S
97466 CCTCGTCAGCTTCGTCCGGTCCGGCGCACCCAACGACATGTCTCAACTGGACAGCTGGAATGAACTGTCCGAACGGGTGGAGCCGGCCGACA
         >  L  V  S  F  V  R  S  G  A  P  N  D  M  S  Q  L  D  S  W  N  E  L  S  E  R  V  E  P  A  D
97558 TCGTCCCGCTCGACGAGGACACCTACGAGCTGGACCTGGTCGTGGAGAACCTGCGGGGTGGGCACGACACCTGGGACTCGGCGCTGCTGATC
         >I  V  P  L  D  E  D  T  Y  E  L  D  L  V  V  E  N  L  R  G  G  H  D  T  W  D  S  A  L  L  I
97650 GAGCCGGCGAGGTGGCCCGGGACGTCGCGTATGCCCTGCGTCTGCCCGCCGTGTTGGACATGTCTCCGCGGTCCAGCCTCGACGACCTG
         >  E  P  A  R  W  P  G  T  S  R  M  P  C  V  C  P  P  C  W  T  C  S  P  P  A  P  A  S  T  T  W
97742 GACGAGGCGCTGCGCGCCACGGCCAACGGCGGGCTCGGGGGCTTCCTCGGCCGCCGGCGGCTGAGGAAAATCGGCGCGCAGACGGCGAGTC
         >  T  R  R  C  A  P  R  P  T  A  G  S  G  A  S  S  A  A  G  G  •
97833 TCGGTTGGCGCACCATTGTCGGCAAGATCTCTGCGGTCGTGGACTGGCGCGACTGACACGTTCCAGGGAGCATCAGTCTCTGGCAGAGAAAG
                                                              BamHI
                                                              junction marker
97925 ACCAGTCCCGGGAGGAGGACGACGCTGTGGCGCTCGTGCGCGTGTACTGCGGTCTGGCCTCGGCGGATCCGGCCGACCGACCGGCCTCGGCC
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Figure 11Z

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98017 GGTTCGGCGCTGACGTCCGCTGTGGTCGACGACGCAGGTCGGCTGCTCCATGTCTGCGAGATCGGCGACGACCCAGCCGGCTACGCTCAGCT
98109 GGTCGTGCTACTCGTGGAGCGGTCGGGCGGGCCGAGCGGGGCTGCGATCGCCGCCGACAGCGACGACCACACGGTCACCTCGCTGCTGAGTG
98201 CCGCCGGGCGTCCACTGGCGATCGCGGACGACGACTCGGTGGACGACTTCGCCGAGCGGTTCGCCGACGACGACTCGCTGGAGGAGATGCA
                                                                                          > M   Q
98292 GTCCGCGCCGGCCGAGCGGCGGGCGGTCGGGCTGGCCCGGGCGCTCCAGGCCGGCGCGCTCTCGGCGGTCACCCTCCCGGCGCCCCGGGATC
       >  S   A   P   A   E   R   R   A   V   G   L   A   R   A   L   Q   A   G   A   L   S   A   V   T   L   P   A   P   R   D
98384 TCGCCGGCTACAAGCAGGTCCTCTCGGCGCACGCCGCGCTCGCCAGCGGCCGGCACTCCGCCGCCGTGGCGCTGCGCGAGGTGCTGCGGGAG
       >L   A   G   Y   K   Q   V   L   S   A   H   A   A   L   A   S   G   R   H   S   A   A   V   A   L   R   E   V   L   R   E
98476 CTCTACCCGGCCGCCCTGCGCGCGTACCCGGACCCGGCCGAGCCGGTCGCCCTGGCCGTGTTGGACGCCCTGCCCGAGCCCGGCATGCTGGG
       >  L   Y   P   A   A   L   R   A   Y   P   D   P   A   E   P   V   A   L   A   V   L   D   A   L   P   E   P   G   M   L   G
98568 CGGGACGATCGCCCGGGGCCGGGAGGTGTCGGTGGCGGCGGACGCCATCGCCGCCCACCTCGCCGCCGACGGGGTGGCCGACGAAGGCAAGA
       >  G   T   I   A   R   G   R   E   V   S   V   A   A   D   A   I   A   A   H   L   A   A   D   G   V   A   D   E   G   K
98660 TCAACGATGCGGTGACCGCGCTGCGGGTCGCCATCGCCGAGACCCCCGCCGCGCGGCGGTCAGCCGGGCGCTCACCTCCGCCGTGGCGGAG
       >I   N   D   A   V   T   A   L   R   V   A   I   A   E   T   P   R   R   A   A   V   S   R   A   L   T   S   A   V   A   E
98752 ACGGTCCGTCAGGCGGTGGCCTCGGTGCGAGCATGCGACGCGGGCTGCGAGGCCCTGGTCGGCGCGCTCGACGCCCGGGTCACCACCCCCAC
       >  T   V   R   Q   A   V   A   S   V   R   A   C   D   A   G   C   E   A   L   V   G   A   L   D   A   R   V   T   T   P   T
98844 CCCGGTGCCGGGCCGGCGGGCCGCCGCCCGCCGGGGCGAGCCGGTCGCCGAGTTGCCCGGCGCCGGCCTGCGCGCACTGCGGCCCACAGAGC
       >  P   V   P   G   R   R   A   A   A   R   R   G   E   P   V   A   E   L   P   G   A   G   L   R   A   L   R   P   T   E
98936 CCGAGCCGGTCCCCGGCCGGCGCAGCCGTCCCGAGCCGGTCCCCGGCGGCAGCCTGCCCGCCCAGCCCCGCCCGCTCGGCCCGCCGCCGGTC
       >P   E   P   V   P   G   R   R   S   R   P   E   P   V   P   G   G   S   L   P   A   Q   P   R   P   L   G   P   P   P   V
99028 GCGCCGGACCCGTCGCCCCGCCGCCGGTCGCCCCGCGCCCGATCACCCCGGCCGCCTCGGCCACCCCGCCGGTCTCCGGCCCGCCGTCGCC
       >  A   P   E   P   V   A   P   P   P   V   A   P   R   P   I   T   P   A   A   S   A   T   P   V   S   G   P   P   S   P
99120 CGAGCCGCGCCGCCTGATCGACAACCCGGCCAACCGGCCGGTCTCCGCGCCGCCACCCCCCGCCACCGGGGATCACCCCGATCGCGCCGAGCC
       >  E   P   R   R   L   I   D   N   P   A   N   R   P   V   S   A   P   P   P   P   P   P   G   I   T   P   I   A   P   S
99212 AGCGCGAGCGCGGGTCCGTGCCGCCGGCCGAGGCCGGTGAGCCGGTTCCGGCCCACGCTGACCACCGCCGCGATCCAGAACGCGCGGGCGGAG
       >Q   R   E   R   G   S   V   P   P   A   E   A   G   E   P   F   R   P   T   L   T   T   A   A   I   Q   N   A   R   A   E
99304 CGGCAGCGCACCATCATCCCGCCTCGCCCCAAGACGACGGGCGAGTCCGCGCCGCCGCCCACCGGCGGCTTCAGCGCCACCGACCTGAGCGT
       >  R   Q   R   T   I   I   P   P   R   P   K   T   T   G   E   S   A   P   P   P   T   G   G   F   S   A   T   D   L   S   V
99396 CCCGGTGCCGACCCCGCGTCCCGGCCAGGAGTCCGCTCCCCCCGGCTCGCGGGCGAACTGGCCGCTGGTCAACAACCCCGAGGACCCCGCCG
       >  P   V   P   T   P   R   P   G   Q   E   S   A   P   P   G   S   R   A   N   W   P   L   V   N   N   P   E   D   P   A
99488 ACAGCTCCCCGAACAATCCCGTCGCGCGGCGGCCCTTGGAGGATCGGGCGAAGCGGCAGATCGACGCGCCGACCCAGGTGGTCCCGCCGGCC
       >D   S   S   P   N   N   P   V   A   R   R   P   L   E   D   R   A   K   R   Q   I   D   A   P   T   Q   V   V   P   P   A
99580 GAGGGCCGGGTCACCCCGCCCTGGCTCGCCGACGACCTGCCCCAGGAGCCACCGATGCTGCGGCTGGTCGAGCCGCCACCGCTGGCCGACCG
       >  E   G   R   V   T   P   P   W   L   A   D   D   L   P   Q   E   P   P   M   L   R   L   V   E   P   P   L   A   D   R
99672 GGCACTGCGGGATGGGCCGGGCCAGGCTGCCGACCCGCGCCTGGAGCCCCCGCCGCTGCGGCTGGTCGACCGCGGCGAGGCAGCCCGCGCCG
       >  A   L   R   D   G   P   G   Q   A   A   D   P   R   L   E . P   P   P   L   R   L   V   D   R   G   E   A   A   R   A
99764 GCCGTCCCGCCGGAGCCCCGCCCCGAGCGGGCCCCCGCGGAACACCGGTCCCCGCTGGGTCAGCGGGTCCCGTTGGAGGAGCGGCCCGAC
       >G   R   P   A   P   E   R   P   E   R   A   P   A   E   H   R   S   P   L   G   Q   R   V   P   L   E   E   R   P   D
99856 ATGGAACATCGGACCGCCCCGCCGCAGCCGTCGCGGTCCGCGCCGATGGAGCGGCGTACCCCGCCGATCTCCGACGAGGGGGACGGCGACCT
       >M   E   H   R   T   A   P   P   Q   P   S   R   S   A   P   M   E   R   R   T   P   P   I   S   D   E   G   D   G   D   L
99948 GCTGATCTTCGCCGCCGCCAAGTCGGCCTGGTTCGTCGGGCACGGCGACGAGTCCGAGATGGACTGGTCGAGCACCGCCGACACCGGGTGGC
       >  L   I   F   A   A   A   K   S   A   W   F   V   G   H   G   D   E   S   E   M   D   W   S   S   T   A   D   T   G   W
100040 AGGCCGCCGAGCAGGCCGCCCGCCCGGCCGTGGGCGCCGATACCAAGGCCGGGTTGCCCAAGCCGGTGCCGCAGGCCAACCTGGTTCGGGC
       >Q   A   A   E   Q   A   A   R   P   A   V   G   A   D   T   K   A   G   L   P   K   P   R   V   P   Q   A   N   L   V   P   G
100132 TCCCCCCTGCGCGAGGAGCGTCCCCTACGGATAGTCCGCGACGCGGCCAGCCTCGCCGAGAACACGACCGGCTACTTCCGGGGGCTGGCGTCG
       >  S   P   L   R   E   E   R   P   L   R   I   V   R   D   A   A   S   L   A   E   N   T   T   G   Y   F   R   G   W   R   R
100224 CGGGCAGGAGATCGGCGGGGTTCGCCGTCGGCGGCCGGCCGGGCCGCGAGGCGGCCGGCGGCTGGGACTTCACCCGGGACACCGGCGACCGAG
       >  G   Q   E   I   G   G   F   A   V   G   G   R   P   G   R   E   A   A   G   G   W   D   F   T   R   D   T   G   D   R
100316 ACGACGACCGGGAGTACGAGTACCGGTCCGCCGGCTACCGCTCCTGACCATCGCGCCGGGGTGGCGGGCACCGCCGCCCCCGGCCGCGCCCG
       >D   D   D   R   E   Y   E   Y   R   S   A   G   Y   R   S   •
100407 CCGTGCTGGCGTACGGCCGTAGCAACCCGACGCCCACCCGACCGACCGGTGGGACCACACCGAAGAGCAACCCTGGCCGGCCGCCTGACGTC
100499 CCGCAGGGACGGTGACGGCTACTGGCCGTCCCCCCGGGAAGGTTGCGAGGCGGTCGGGGCGCACAGGCGCTGTCAGGGCCGCTCCTGAGCCG
100591 CCCTACGGAATGGGCTAGCCCTACGGAATCGAGCGCCGGCCGCCCGCCGGTGGCGTCGAGTTCGCCTCCAGCCGGTCCCCAAACAGCCGGAC
100683 GCGCCCGACGGCCCGGCGGGTGCCGGTCGTCGGGCGCGTCCCGTCGTCGATCAGGCCGGCGCGAGCCGGCGAGCCGGCATCGTGAGCA
                                                        <  • A   P   A   V   A   R   S   R   R   M   T   L   V
100774 CGTACTCGACCAGCGAGATCAGCACGTGCTTCGTCGACTCCCGGTTCGGGCGTCGCAGGCCACCACCGGCACGTCGTGCGAGATCGCGAGC
       <  Y   E   V   L   S   I   L   V   H   K   T   S   E   R   N   R   A   D   C   A   V   V   P   V   D   H   S   I   A   L
100866 GCGTCCCGGACGTCCTGCGGGTCGTGGTACTGCATCCCGTCGAAGCAGTTGATGGCCACCAGGTACGGCAGCCGCCGATGCTCGAAGAAGTC
       <A   D   R   V   D   Q   P   D   H   Y   Q   M   G   F   C   N   I   A   V   L   Y   P   L   R   R   H   E   F   F   D
100958 GATGGCCGCGAAGCAGTCGGCCAGCCGCCGGGTGTCGACCAGGACCACCGCCGATGGCGCCCGGACCAGCCTCGTCCCACATGAACCAGA
       <  I   A   A   F   C   D   A   L   R   R   T   D   V   L   V   V   A   G   I   A   G   R   V   L   E   D   W   M   F   W   F
101050 ACCGGGTCTGGCCGGGGGTGCCGAACAGGTACAGGATCAGGTCCCGGTCGATCGAGATACGGCCGAAGTCCATCGCCACCGTGGTCGTCGTC
       <  R   T   Q   G   P   T   G   F   L   Y   L   I   L   D   R   D   I   S   I   R   G   F   D   M   A   V   T   T   T   T
101142 TCGCCCGGCACCTGCCGGGTGTCGTCGACGCCCACGCCGGCGGAGGTCATGATCGCCTCGGTGGTCAGCGGCGTGATCTCCGAGACCGAGCC
       <E   G   P   V   Q   R   T   D   D   V   G   V   G   A   S   T   M   I   A   E   T   T   L   P   T   I   E   S   V   S   G
101234 GACCAGCGTCGTCTTCCCGACGCCGGAACCCACCGGCGATAACGATCTTCGCCGACGTCACGCCGCCGCTCGGGACAGGCGGGCGGTGCGACA
       <  V   L   T   T   K   G   V   G   F   G   G   A   I   V   I   K   A   S   T   V   R   G   S   P   V   P   P   R   H   S   M
101326 TGTCAGAGCCTGCGAAGTCCACTCAGCACCCTCTCCAGCAGTTCAGTGCCCACCGCGTCGTCGGAGTCGTCCAGGATGGTCGGCTCGTGGA
       <  <  •  L   R   R   L   G   S   L   V   R   E   L   L   E   T   G   V   A   D   D   S   D   D   L   I   T   P   E   H   V
101417 CTGCGACCAGGCCGTCCGTCGCCATGTCGGCGATGAGCACCCTAGCCACGCCGAGCGGGAGCTGCATCCGCGCCGGGATCTCGGCAAGCGAC
       <  A   V   L   G   D   T   A   M   D   A   I   L   V   R   A   V   G   L   P   L   Q   M   R   A   A   I   E   A   L   S
101509 TGCACGCGTCCGTCGCACAGCGCGGCGATGTACTGGTGCTCTCGGCCCTGGCCACCGTTGCTACTGGCAGCGGCCCGACCGGCACCGTCGT
       <Q   V   R   G   D   C   L   A   A   I   Y   Q   H   E   R   G   Q   G   G   N   S   S   A   A   A   R   G   R   V   T   T
101601 CTCGACGAGCGCCTCCAACGCGATGTCCAGCCGAGGGCGGGTACGACCGCGGGTGACGGCGTACGGACGGACCAACGCGCCAGTCGGCTCGT
       <  E   V   L   A   E   L   A   I   D   L   R   P   R   T   R   G   R   T   V   A   Y   P   R   V   L   A   G   T   P   E   D
101693 CACGATCCATGTCGACGGTCTCACCTCCTTCGTCCCCGACACCGGCTGAACCCGGTGGAACCCGTCGTTCTTGTCCTTGCCACCCCGCCCGAC
       <  R   D   M   D   G   S   V   E   K   T   G   S   V
101784 CCATCGGCCAGCGCGTGGGTCAGCCCATCATCCCCACAGTCGTACGCGGCTGCGGGGTCAACGCGTCGCCCACCCGGTCGACCAGGAGGGC
                                     <  •  G   M   M   G   V   T   T   R   P   Q   P   T   L   A   D   G   V   R   D   V   L   L   A
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Figure 11AA

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101875 CATCTCGTATCCGACCTGCCCGACGTCGCAGCTACGGGCGGCGAGCACGGCGAAGGACGAGCCGTCCGAGATGGACATCAGGAACAGGAAGC
       < M  E  Y  G  V  Q  G  V  D  C  S  R  A  A  L  V  A  F  S  S  G  D  S  I  S  M  L  F  L  F  G
101967 CGTTGTCCATCTCGACCACGGTCTGCAGCACCGCACCGCCCTCGAAGCAGCGTGCCGCTCCCTGCGTGAGGCTGACCAGCCCGGACGCGATC
       < N  D  M  E  V  V  T  Q  L  V  A  G  G  E  F  C  R  A  A  G  Q  T  L  S  V  L  G  S  A  I
102059 GCGGCGAGCTGGTCGGCCCGGTCACGCGGAAGGTCTCGTGACGACGCCAGGAGCAGACCGTCCGCGGAGCGGCGACCGCGTGCGCGACACC
       <A  A  L  Q  D  A  R  D  R  P  L  D  R  S  S  A  L  L  G  D  A  S  V  A  V  A  H  A  V  G
102151 GGGCACCCGGTCGGCGAAGTTGGCCAGCAGCCAACCGAGATCCTGCGTAGTTGTCATCCTTGTTGCTCCTTCTGCCCGCTCCCGGCCACCG
       < P  V                                              <  °  G  Q  Q  E  K  Q  G  S  G  A  V  P
102242 GGCCTGAGCCAGACTGCGAGGATTGCTGCCCACCCGGAGCTGCCTCCGGGTTGGTCGGGTTGCCGTCGGGCTCGGTACGCCCACGCTGCACG
       < G  S  G  S  Q  S  S  Q  Q  G  G  P  A  A  E  P  N  T  P  N  G  D  P  E  T  R  G  R  Q  V
102334 CCTCGATGGTATGCCGAGAGCAGACCGGGACGCCCTCCGGCGTACGGCGCTGGACCGACGTGGTGGGCTTCTCCACCCCGCCAGGCACGAG
       <G  R  H  Y  A  S  L  L  G  R  V  G  E  P  T  R  R  Q  V  S  T  T  P  K  E  V  G  G  P  V  L
102426 TTGGGCCATCGGCACCCGCTTCGGCAGGCCCTTGCGGGTGGTCTCCGCCACCGGGACCTCGGTGGCCGCCGAGGCGGCCCGCCAGCCGTCGT
       <Q  A  M  P  V  R  K  P  L  G  K  R  T  T  E  A  V  P  V  E  T  A  A  S  A  A  R  W  G  D  D
102518 CCGCGGCAGTCTGCCCAGGCGTGGGCCTGCGGCGTGGGCCGCCGGCGAAGCCCTCGGCGGGACCGGGGCGGGTGCCACCGTTGGTCGGC
       < A  A  T  Q  W  A  H  A  Q  P  T  P  R  R  G  A  F  G  E  A  P  G  P  R  T  G  G  N  T  P
102610 GACCCGTTGTCGCGCGGCATTCCTCCGGCCATCGGGGTGTCTGCCATCGGTGCGTTACCTGTCGTCCCGGGTGCTGGTGTCTGGACGGGCC
       <S  G  N  D  R  P  M  G  G  A  M  P  T  D  A  M  P  A  N  G  T  T  G  P  A  P  T  Q  V  P  R
102702 GCCGGTGACGTCGACCGCGGAGAACTGTTGGGTCACGGCGGCGTTCGCCGGGCTCCCGGCGCCATTGGTCGCGCGCTGGGCGACGCCGGCCG
       < G  T  V  D  V  A  S  F  Q  Q  T  V  A  A  N  A  P  S  G  A  G  N  T  A  R  Q  A  V  G  A  T
102794 TCTCCTCCGAACCCGAGCGGGTACGGAACCAGGCCGACTCGAGCTCCCGGAAGATCGGCAGCTCCATCGTCTCGTCCGCGTACCGCTGC
       < E  E  S  G  S  R  R  T  R  F  W  A  S  E  L  E  R  F  I  P  L  E  M  T  E  D  A  Y  R  Q
102886 TGCCGGTTCTGGGCCTGCACGGGCGTCGACCGCGCCGGCGTGGGCGGGGTCGTCGGCTGGGTGGCCGGCGTGCTCGGCACCTCGGTGCTCGG
       <Q  R  N  Q  A  Q  V  P  T  S  R  A  P  T  P  P  T  T  P  Q  T  A  P  T  S  P  V  E  T  S  P
102978 CACCCGGGGGCAGCTCCGTGGTCATGTCCAGGGCTGCGGCGAGGCGCTCCGGCACCGGCGGGGTGACCGGCTCCGGCGCGGCCACCGGCGGCC
       < V  R  P  L  E  T  T  M  D  L  A  A  A  L  R  E  P  V  P  P  T  V  P  E  P  A  A  V  P  P  W
103070 AGGCCGGCGGCGCCACCGGGCGCCTGGGCCGGCAGACCGGCCGGCGACTGGGCAGCGGCTGCGCCGAGTACGGCTGCGACCGGACGGCCG
       < A  P  P  A  V  P  A  Q  A  S  P  V  P  R  S  P  L  P  Q  A  S  Y  P  Q  G  S  V  P  T  G
103162 AACGGCTGACCGGAGACGGGCGTGCCGAACGGCTGACCGGACACCGGGCGGCCGAGACGGGCTGACCCGAGACCGGGAAGACGGAAACCGG
       <F  P  Q  G  S  V  P  T  G  F  P  Q  G  S  V  P  A  A  S  V  P  Q  G  S  V  P  F  V  S  V  P
103254 CGGTGCGGACACCGGCGGCACCGAGACCGGTGGCGGGGTCCAGCCCCGGGCCTCCGGGCTGCTCGGCAGCTGTCGGGGGATGGCCGGCTGCT
       < P  A  S  V  P  V  S  V  P  P  P  T  W  G  R  A  E  P  S  S  P  L  Q  R  P  I  A  P  Q  Q
103346 GGCCGCTGCTGGCCGGATCCGGCGTCGCCGGACGCCCGCCGCTGCGGCAGCGGGTCGCTCGACTGGCCATTCGAGGTGCGGCCGGCGGCGGCA
       < G  S  S  A  P  D  G  D  G  S  A  R  R  Q  P  L  P  D  S  S  Q  G  N  S  T  R  G  A  A  A
103438 CCGCCAGCGGTGCCACTGGCCCCGGTCAGGTCCGACCAGGCCGGCATCGACCGCATGGAACCGGTCGACGCGGGCGTGCCGTGGCCGTTGCG
       <G  G  A  T  G  S  A  G  T  L  D  S  W  A  P  M  S  R  M  S  G  T  S  A  P  T  G  H  G  N  R
103530 CGAGGCCGGGTCGAACGACCGGCGCCCCCAGGGTTACCTGGTTGCCCGAGTGCCCCGGCCGCTGGGTGGGCGCCGGTGTCGCCGGGTTGTTGC
       < S  A  P  D  F  S  R  G  G  L  T  V  Q  N  G  S  H  G  P  R  Q  T  P  A  P  T  A  P  N  N  G
103622 CGAAGGCCGCGAAGGCACCCAGGGCGCGGGGGGCCCCGCCGGGCTGCGAGCTGGTGAGCGAGGCGGGAGGGGCCGGCAGCGGCGCCGGGCTGC
       < F  A  A  F  A  G  L  A  P  P  A  G  G  P  Q  S  S  T  L  S  A  P  P  A  P  L  A  G  P  Q
103714 TGGAACCGGCCGGAGAGCGCCCGGGGCACCAGCACGGTGGTGGGCAGGGTGACGTCGGCGACGGTCCCCCGGTCGGTGCCGGGCCGCAGCTC
       <Q  F  R  G  S  L  A  R  P  V  L  V  T  T  P  L  T  V  D  A  V  T  G  R  D  T  G  P  R  L  E
103806 GACCTTGACCCCGTGCCGGGACGACCAACCGGGCGACCACAACCAGGCCCATCATCCGGGAGACGGCCACGTCCACCTGCGGCGGCGAGGCGA
       < V  K  V  G  H  R  S  A  L  R  A  V  V  V  L  G  M  M  R  S  V  A  V  D  V  Q  P  P  S  A  L
103898 GGCGGTCGTTGAGGTCGTGTAGCTGCTCGGCGCTGATGCCGATGCCCCGGTCCTCGACGTAGAGGTTGGCCGGTCGCCGACCCGGCGGGCC
       < R  D  N  L  D  H  L  Q  E  A  S  I  G  I  G  R  D  E  V  Y  L  N  A  R  D  G  V  R  R  A
103990 TCCACCATCACCTGCGAGTCGGGCGGCGAGAAGGCGGTCGCGTTGTCGAACAGCTCGGCGACCAGGTGGACCAGGTCGTTGACCGCGTGCGC
       <E  V  M  V  Q  S  D  P  P  S  F  A  T  A  N  D  F  L  E  A  V  L  H  V  L  D  N  V  A  H  A
104082 GGCGACCTCGATGTCACGGTCGATCACCCCGAACTCGATCGGGTGTAGTGCTCGACCTCGGACTGGGCGGCCCGCAGCACGTCGATCAGTG
       < A  V  E  I  D  R  D  I  V  G  F  E  I  R  T  Y  H  E  V  E  S  Q  A  A  R  L  V  D  I  L  A
104174 CCGCCGGCTCGCGCTGCACGCGGGTGGAGTCGGCCCCGGCGAGCACCAGCAGGTTCTCGTCGTTGCGGCGCATCCGGGTGGCCAGGTGGTCG
       < A  P  E  R  Q  V  R  T  S  D  A  G  A  L  V  L  L  N  E  D  N  R  R  M  R  T  A  L  H  D
104266 AGCTGGAACAGCTCGGCCAGCCGGTCCGGGTCCTCCTCGCCGCGCTCCAGCCGGTCGAGGTGGCCGATCAGCCGGTCGACCAGGATCTGCGA
       <L  Q  F  L  E  A  L  R  D  P  D  E  E  G  R  E  L  R  D  L  H  G  I  L  R  D  V  L  I  Q  S
104358 ACGGCGGGCCAGGTTGACGAACATGGTCGCGACGGAGGCGCGCAGCGCGGCCTGCTCCGCGCCGTCCGTACGGCGTCCAGGTGGACCGCGT
       < R  R  A  L  N  V  F  M  T  A  V  S  A  R  L  A  A  Q  E  A  A  T  R  V  A  E  L  H  V  A  N
104450 TGAACGCCTCGGTCACCTGGCCGAACTCGTCCTTGCTGCGCACCGGCAGCGGCTCGGCGATCTGGTTGGCCGCCTGCACCGGGGAGAGCTGG
       < F  A  E  T  V  Q  G  F  E  D  K  S  R  V  P  L  P  E  A  I  Q  N  A  A  Q  V  P  S  L  Q
104542 CTGGAAAACTGCGGATCGCGCAGCCGGGCAACGGCCTGGGGCGACTGGGCGATGCTGAGCGCACCCTGGCGCAGGTCGCGCAGCGA
       <S  S  F  Q  P  D  R  L  R  A  V  A  Q  P  L  G  Y  Q  A  I  S  L  A  G  Q  R  L  D  R  L  S
104634 GCGGGCCATCGACCGGGCGACCAGGTACGCGAACAGGATGGCCAGCAGCAGCATGCCGAGCAGCAGGCCGGTCTGGAGGAACACCGTGCGCT
       < R  A  M  S  R  A  V  L  Y  A  F  L  I  A  L  L  L  M  G  L  L  L  G  T  Q  L  F  V  T  R  Q
104726 GTACGTCGGAGCGGAGCGCGTCGGCCTGCTTGACCACGTTGCCGTCGAGCTTCGCCTCGACCGTACGGATCAGTTTGGCGCTGGCGACCATG
       < V  D  S  R  L  A  D  A  Q  K  V  V  N  G  D  L  K  A  E  V  T  R  I  L  K  A  S  A  V  M
104818 GCCGCGTCCCACTGATCCGGCCCGAACGGCGCGTTGGCCATGCTGCCGTTGGTGCCGTCGAGCCAGCCGGTGTAGTTCTGCGCCTCGGCG
       <A  A  D  W  Q  D  P  G  F  P  A  N  A  M  S  G  N  T  N  G  D  L  W  G  T  Y  N  Q  A  E  R
104910 CCGGTCGCCGCCGGCGACGGTCTGGTCGTGCAGGTCCGACTCGTCCAGGCTGGCCACCGCCTTGAAGCTTTGCAGTGCCTGCTGCTGGCCGG
       < R  D  G  G  A  V  T  Q  D  H  L  D  S  E  D  L  S  A  V  A  K  F  S  Q  L  A  Q  Q  Q  G  T
105002 TGCCGGCGATGTAGTCGGTGCGCAGGATGGGGGTCAACTCGCGCTGGATCAGCGCCCGGTGCACCACGACCCGGCGGACCGAGAGGTAT
       < G  S  A  I  Y  D  T  R  L  I  P  T  L  E  R  Q  I  L  A  R  H  V  V  V  R  R  V  S  L  Y
105094 TCCTTCTCCCGGGCGACGGCTGCCGCGGCCCGCATCCGGTCGCTGCTCAGGTCGTTGTCACCGGCGAGGTGGGTGGGGAGTCGCGGATGGACAG
       <E  K  E  R  A  V  A  A  A  A  R  M  R  D  S  L  D  N  D  G  A  L  H  T  A  S  D  R  I  S  L
105186 CAGGTCGTTGATCAGGCCCTCGTACGCCTGCATGGCGTCGATGATCTTCAACTTGCCGTTGAAGACCTGGCTGCGGGTGCCGGGGAGGTCCT
       < L  D  N  I  L  G  E  Y  A  Q  M  A  D  I  I  K  L  K  G  N  F  V  Q  S  R  T  G  P  L  D  K
105278 TCAGGTTCGTGATCCCGTCGAGGAGGCCCTCCAGGCTGCTCGGCAGGCCGTCGACCTCCCCCCGCTGTTGCAGGTACGGCACCTTGTCC
       < L  N  Q  D  L  L  G  E  L  S  S  P  L  G  D  V  E  G  R  Q  Q  L  Y  P  V  K  D
105370 TGGTCGACCCGGATGTTGACCCGGTTGTACGCCTCCTGGTACTGCGCCTTGGCCTGGTCGCCGCTCGCCCCGAGCAGCAACACCGGGAGGT
       <Q  D  V  R  I  N  V  R  N  Y  A  E  Q  Y  Q  A  K  A  Q  D  G  S  A  G  L  L  L  V  A  S  T
```

Figure 11AB

```
105462 GCGTTCGTCCTGGAGGCTGTTGACCAGGTCGCCCGAGTAGCCCACCAGATTGGCCAGGTCGCCGGAGCGGTTGGCGTTGTTCAGCGTTTCCA
        < R  E  D  Q  L  S  N  V  L  D  G  S  Y  G  V  L  N  A  L  D  G  S  R  N  A  N  N  L  T  E  L
105554 GGTTGTCGACGAGGCCACTGGTGCCGACGACGACCGTGGCGATGGTCGGCACGATCATGATGAGACCGAGCTTGGACCAGATCGGCATGTC
        < N  D  V  L  G  S  T  G  V  V  V  T  A  I  T  P  V  I  M  I  L  G  L  K  S  W  I  P  M
105645 GCGGAGCCGGCCGACCGGCCGACGCAGTCGCGACAGGAAGGAACCCGCCGTCTTCGGTCGTTTGCTCACGTCACCGCCCTCGCGATCACAGC
105737 GTTCGCGCGTTGCCCCGGGCAACGCTCAGCGACCGACCCGGCGGGTCGGACCTCCGAGATTCCATCACGCCGTGTTCCAAAGAGAAAGCCCA
105829 GGCTGGCCGTCGCCGGAGGTGTGATGAGATGTTGATGCAATTTGCTCGCAATCCGTCCAGCCGGAGTGACTGACAGTAATGGATCACCCC
                                                                            > M  D  H  P
105919 CACCGCCTCGTCCTGCTCGCCGGCCCTTCGGGCTCCGGAAAGTCGTACATAGCCCAACAAACCGGGCTTCCTGTTCTTTGTCTGGACGACTT
        > H  R  L  V  L  L  A  G  P  S  G  S  G  K  S  Y  I  A  Q  Q  T  G  L  P  V  L  C  L  D  F
106011 CTACAAGGATGGTGATGACCCTACGTTACCGCCCAAAACGGTCTTGTGGACTGGGACTCACCCCAGTCGTGGGACGCGGGGCGGCCGTGG
        > Y  K  D  G  D  D  P  T  L  P  R  Q  N  G  L  V  D  W  D  S  P  Q  S  W  D  A  G  A  A  V
106103 AAACGATTGCCCGGCTGGCGCGGGACGGCAAGGCCGAAGTGCCGGTTTATGCGATCGGCGCGGACCGGCGGGTGGCCACCCGGACATTCGAG
        >E  T  I  A  R  L  A  R  D  G  K  A  E  V  P  V  Y  A  I  G  A  D  R  R  V  A  T  R  T  F  E
106195 GTCGCCGGATCGCCACTTTTCGTCGCCGAAGGGATTTTCGCCGCCGAGATCGTCGAGGAATGCCGACGGCGAGGGCTGCTCGCCGGGGCGTA
        > V  A  G  S  P  L  F  V  A  E  G  I  F  A  A  E  I  V  E  E  C  R  R  R  G  L  L  A  G  A  Y
106287 CGCGCTGCGCCGGCCGCGCGGCACCACCTTTTTCCGGCGGCTCGCCCGCGACCTGGCCGAGCAGCGCAAGGCTCCCGGGATGCTGCTGCGGC
        > A  L  R  R  P  R  G  T  T  F  F  R  R  R  L  A  R  D  L  A  E  Q  R  K  A  P  G  M  L  L  R
106379 GCGGCCTGGCCCTGCTGCGCGCGGAGCCGGCGGTGCTGCGCCGCCAGGCGGGGCTCGGCGCTCACCCGGCCCCGGCCCGCGAGGTGCTGCGC
        >R  G  L  A  L  L  R  A  E  P  A  V  L  R  R  Q  A  G  L  G  A  H  P  A  P  A  R  E  V  L  R
106471 CGGGTGGCCGACCTGCTCGCCGGGCCACCCGCACCACCCCTGATCAGCCGACGCAGCTTCCCGTACGCCGGCTTGATCACCTCGTCGATGAT
        >R  V  A  D  L  L  A  G  H  P  H  H  P  •  •  G  L  L  K  G  Y  A  P  K  I  V  E  D  I  I
106561 GGCCAGCCGCTCGTCGAACGGGATGAACGCGCTCTTCATCGGTTGATGGTGAACCATTGGAGCTCCTTCCAGCCGTAGCCGAAGGCCTCCG
        < A  L  R  E  D  F  P  I  F  A  S  K  M  A  N  I  T  F  W  Q  L  E  K  W  G  Y  G  F  A  E  A
106653 CCAGCAGCGCCATCTCCCGGGACATCGAGGTGCCGCTCATCAGCCGGTTGTCGGTGTTCACCGTCACCCGGAACCGCAGATCGCGCAGAAGC
        < L  L  A  M  E  R  S  M  S  T  G  S  M  L  R  N  D  T  N  V  T  V  R  F  R  L  D  R  L  L
                                        BamHI
                                        junction marker
106745 CCGATCGGGTGCTCGGCGATCGACGCCGCCGCGCCGGTCTGCACGTTCGACGACGGGCACAGCTCCAGCGGGATCCGCTTGTCCCGCACGTA
        <G  I  P  H  E  A  I  S  A  A  A  G  T  Q  V  N  S  S  P  C  L  E  L  P  I  R  K  D  R  V  Y
106837 CGCCGGCCAGCCGGCCCAGCACGGGCGGGTCGCCGGGGGTGATGTCGTCCACGATGCGCACCCCGTGGCCGAGGCGGTCCGCGCCGCACCACT
        < A  A  L  R  G  L  V  P  P  D  G  P  T  I  D  D  V  I  R  V  G  H  G  L  R  D  A  G  C  W  Q
106929 GGATGGCCTGCCAGATCGACGGCAGCCCGAACGCCTCGCCGGCGTGAATGGTGAAGTGGAAGTTCTCCCCGCTGCAGGTACTCGAAGGCGTCC
        < I  A  Q  W  I  S  P  L  G  F  A  E  G  A  H  I  T  F  H  F  N  E  R  Q  L  Y  E  F  A  D
107021 AGGTGCCGGGTGGGCGGGAATCCCGCCTCCGCCCCGGCGATGTCGAAGCCCACCACGCCGGCGTCGCGGTGCCGCACCGCCAGTTCGGCGAT
        <L  H  R  T  P  P  F  G  A  E  A  G  A  I  D  F  G  V  V  G  A  D  R  H  R  V  A  L  E  A  I
107113 CTCCTGCGACCGGGCGGCGTGCCGCATGGCGGTGAGCAGGGTGCCGACCCGGATCGGATGGCCGGCGTCGGCGGCGAGCGCCGCGCCCTCGG
        < E  Q  S  R  A  A  H  R  M  A  T  L  L  T  G  V  R  I  P  H  G  A  D  A  A  L  A  A  G  E  A
107205 CGAACCCGGCGACGACCGCCTCGACCACCTCGTCCAGGGTCAGGTCCCGCTCCAGGTGCTGCTCGGGGCGGGAACCGCACCTCGGCGTAGACG
        < F  G  A  V  V  A  E  V  V  E  D  L  T  L  D  R  E  L  H  Q  E  P  A  F  R  V  E  A  Y  V
107297 ACCCCGTCGGCGGCCAGGTCCAGCGCGCACTCCTGGGCCACCCGCCGCAGTGCGGGCGCGGTCTGCATGACCGCCACGGTGTGGGCGAACGT
        <V  G  D  A  A  L  D  L  A  C  E  Q  A  V  R  R  L  A  P  A  T  Q  M  V  A  V  T  H  A  F  T
107389 CTCCAGGTAGCGCTCCAGCGAGCCGGAGTTCGCCGCCGCGACGAACCAGCGGCCGAGCGCTTCCGGGTCGGTGGTGGGCAGCTCGTGGCCGA
        < E  L  Y  R  E  L  S  G  S  N  A  A  A  V  F  W  R  G  L  A  E  P  D  T  T  P  L  E  H  G  V
107481 CCTCGGCGGCCAGCTCGACGATCGTCGCCGGCCGCAGGCCGCCGTCGAGGTGGTCGTGCAGCAGCGCCTTGGGGACCTTGACGATGTCCTCG
        < E  A  A  L  E  V  I  T  A  P  R  L  G  G  D  L  H  D  H  L  L  A  K  P  V  K  V  I  D  E
107573 TATGAGATTGCGACCATGCCCAGACCCTAGTAGCGACCGGCCGGGTCGCCGACGCGACCGGCTGGAGGATGTCCAGGTGATGGACCCC
        <Y  S  I  A  V  M
                                                                            > M  D  P
107662 CGCATCGTCGACCGGCTGCGTTGCCCGGTCTGCGCGGAACCGCTCACCGAGGCCGCCGCCGGGACCACCCGGGCGCTGCGCTGCCCGCGCCG
        > R  I  V  D  R  L  R  C  P  V  C  A  E  P  L  T  E  A  A  A  G  T  T  R  A  L  R  C  P  R  R
107754 GCACAGCTTCGACGTGGCCCGCCAGGGGTACGTCGACCTGCTCGCCGGCCGGGCCCCGCACGTGGGCGACACCGCCGAGATGGTGGCCGCCC
        > H  S  F  D  V  A  R  Q  G  Y  V  D  L  L  A  G  R  A  P  H  V  G  D  T  A  E  M  V  A  A
107846 GCGCCGACTTCCTCGCCGCCGGGCACTACGACACGCTCTCGGCCGCGCTCGCCGCCGCCGCGCTCGCCGCGCTGAGCCACCCGCCGGAGGCC
        >R  A  D  F  L  A  A  G  H  Y  D  T  L  S  A  A  L  A  A  A  L  A  A  L  S  H  P  P  E  A
107938 CCCGGGAGCGGACGCGTCGGCCGGCAAAGACGGGCAGGATGCCCAAGCCGGGCGGGATGCGTCCGCTGGACATGACGCGTCCGCCGGACAGCC
        > P  G  A  D  A  S  A  G  K  D  G  Q  D  A  Q  A  G  R  D  A  S  G  H  D  A  S  G  Q  P
108030 GGCCGTCGGGACGTACCCGCTGGTGGTGGACGCCGGGGCGGGCACGGGCCGGCACCTCGCCGCGGGTGCTGGCGGCGCTGCCCGACGCCGTGG
        > A  V  G  T  Y  P  L  V  V  D  A  G  A  G  T  G  R  H  L  A  A  V  L  A  A  L  P  D  A  V
108122 GCCTGGCCCTGGACGTCTCCAAGCCGGCGCTGCGCCGGGCAGCGCGGGCCCACCCGCCGCGGCGGCCGGCGTCGCCGACACCTGGCGGCGG
        >G  L  A  L  D  V  S  K  P  A  L  R  R  A  A  R  A  H  P  R  A  A  A  A  L  A  D  T  W  R  R
108214 CTTCCGCTGGCCGACGCCAGCGTCGCCGTGCTGCTCGACGTCTTCGCCCCGCGCAACGGCGCGGAGTTCCGCCGGGTGCTCCACCCGGCCGG
        > L  P  L  A  D  A  S  V  A  V  L  L  D  V  F  A  P  R  N  G  A  E  F  R  R  V  L  H  P  A  G
108306 CGCGCTGCTCGTGGTCACCCCCGCCGAGGACCACCTCGCCGAACTGGTCGACTCGCTCGACCTGCTGAAGGTCGACCCCGACAAGGCGGACC
        > A  L  L  V  V  T  P  A  E  D  H  L  A  E  L  V  D  S  L  D  L  L  K  V  D  P  D  K  A  D
108398 GGGTCGCCGGGAGCCTGGCCGGCACTTCGAGACCGCCGAGAGCGTGCTGCGGGCCCGGCTGGAACTCACCGGCCGGCAGGTGGCCACC
        >R  V  A  G  S  L  A  G  H  F  E  Q  T  A  E  S  V  L  R  A  R  L  E  L  T  G  R  Q  V  A  T
108490 CTGGTCGGGATGGGACCCAGCGCCTGGCACACCGACCCGGCCACCCTCGCCGCCCGGATCGCCGCGCTACCCGAGCCGGTCCGGGTGACCCT
        > L  V  G  M  G  P  S  A  W  H  T  D  P  A  T  L  A  A  R  I  A  A  L  P  E  P  V  R  V  T  L
108582 CGCGGGTACGGCTCGGCGTGTACCGCCCCCGCTGACCGGGGCGCGGCCCGCCGCTCAGGTGGAAAGGTCGACCTCTTCCCAGCCCGGCGGCTC
        > A  V  R  L  G  V  Y  R  P  R  •            < •  T  S  L  D  V  E  E  W  G  P  P  E
108674 CTCGTGGTAGGGCCCTCGCAGGACCACCGCCCACTCCAGCGCCCACCGGCGTGCCCGATCGGTTGGCGTCGACCAGGCCGGGCGGCGACC
        < E  H  Y  P  G  R  L  V  V  A  W  E  L  A  W  R  R  G  I  A  N  A  D  V  L  G  P  P  S  R
108766 GCCCGTCGCGCTCCAGCTCCAGGTACGCCCAGTCGAGGCAGTAGTGCAGGTCGAGCAGGGCCGCCGCGTCGGCCGGGTGCTGGGGCGCGGCC
        < G  D  R  E  L  E  L  Y  A  W  D  L  C  Y  H  L  D  L  L  A  A  A  D  A  P  H  Q  P  A  A
108858 AGGATGGGGAGCGCCACTGCTGGAAGCTCTCCCCGCCCGCGATGTGCGGCAGCCGCTCCACCAGCCGCTCGTCGACCGGCAGCGTCGGGTC
        <L  I  R  S  R  W  Q  Q  F  S  E  G  G  A  I  H  P  L  R  E  V  L  R  E  D  V  P  L  T  P  D
108950 GAGCTGCTTGGCCAGGCCGAGCACCCAGGCCAGCGAGAACAGCGCGTCGTGGTGCAGCAGCGAACGACCGGTGGTCGCCCCGGCCGCCCATCA
        < L  Q  K  A  L  G  L  V  W  A  L  S  F  L  A  D  H  H  H  L  V  F  S  R  H  D  G  R  G  G  M  V
```

Figure 11AC

```
109042 CGAACTGCCACTCCGGCGGGGTGACCAGGTCGACCAGGTGGGAGTTGAGCAGCCAGCTCATCGCCGCCTGCGCCGGCATGCCGAAACACCGG
        <   F   Q   W   E   P   P   T   V   L   D   V   L   H   S   N   L   L   W   S   M   A   A   Q   A   P   M   G   F   C   R
109134 GCCAGGATCACGTGCAGCACGGCGATGCGCGCCTCGATCTCGACGGTCGGCCGCAGCTCGATCTCGTCGCCCGGCTCCCACACCAGGGGAA
        <A  L   I   V   H   L   V   A   I   R   A   E   I   E   V   T   P   R   L   E   I   E   D   G   P   E   W   V
109225 ACTGGCTCGGTGGCAGCGGCAGCCCCAGCCGGGACAGCTCGTCCAGGCTGGCGTCACGGACCTCTCGCGGGTCGGGAGCGGAAACGCGCACG
109317 GCTCAGATCCCTGTCAGTCGCATCGGCTCAGTGCCGGTCGTCCCCCTTGGCCTGGGAGGATAGCGGTTCACGACGAGCGGCACCACGGCGGG
109409 CGGGGGCGGGGGCGGTTCAGCCGATCCGCTCGATGACCAGCGGCTGCGGGGTCGGGGCGGTCGGCGAGATCCGTACCGCCCGGACCGCCTCG
                 BamHI
109501 GCCAGCGCCGCCGGGATCC
```

Figure 11AD

```
   1 GTCTTCGGGGAACGCCACGGGGAACCTCCTCGCCAGAACCGGACGAGCTGACCGTAACCGGTGGCACCG

 122 ACGCACCGCCCCGGTGTGAGAAGGGGACCCATCTCTACCGTAGGCGTTAACAAGGGGCCCTTCCTT TCA
                                                                        <  •  R   L   H   L   V   D   G   A   A   L   T   R

 228 CGG GCC CGC CCG GGT GTC GAC CAG CAG CCG GCC GTC CAC GCC GGT CGC CTC CGC ACC GCC GGG GCG GTC CAG CAC
      < P   G   A   R   P   V   D   V   H   L   R   A   D   V   G   T   V   E   A   G   G   A   H   R   W   R

 318 CCG GCC CGG TCT GCC GAC CGT GCG CCC GCG GTC GCC GAC GGC GGC GAG CTG CGG GGG CTG GTC GCG CCA GCG
      < R   V   P   R   G   V   D   A   V   D   R   T   A   C   A   Q   L   A   Q   L   Q   D   P   Q   D   P

 408 GTC GTA CCA CCA GTC GGT GAC GCC GGT GGT GTT GAG GAC GTT GCC GAG CCC GGC GGC GGA CTG CGA GGT GGC
      < D   Y   W   D   A   V   N   D   R   T   V   D   A   V   G   A   L   Q   L   S   T   A   GGT

 498 CGG CAG GCC GGT CGG GTT CGC GGC CTC GTC CAG GTT GAG ACC GAT GCG CGG GGG CTG GTC GTC CGG
      < P   L   G   T   P   N   A   R   L   E   D   V   N   L   G   I   A   P   Q   D   P   CAG

 588 GGC CGG GCC GGG CAC CGC GTC GCA CTC GGG CAG GTT CCA TGG AAG CTG GGC GGC GTC GTC CCA L
      < A   P   G   P   V   A   E   L   R   A   C   W   N   P   W   K   L   A   A   D   CCA

 678 CTC CGC GGG CAG CCG CCG GAC CTC GTA CCC GGT TAC GGG CGG CGC CCG GCC CCG GCG CCG
      < E   A   L   R   A   V   E   V   G   Y   G   G   A   P   P   A   P   R   R   W   D

 768 GCG CTC CGC GAC AGC CTC GCC CTC CGA CTG GGT TCC GCC GCC CTC GAC GTG CGC CGA GGC
      < R   E   A   V   A   R   P   S   Q   W   V   H   A   E   A   V   R   R   G

 858 CCG GCC GGC GGT CTG CCG GGC CGC GAT ATC GTC GCC GCG GCG CAG CAG CGG CGG GTT GGT CGA GCC
      < R   G   A   T   Q   R   E   A   I   V   V   D   A   E   P   A   N   T   S   G

 948 GGT CTC GGC GCG TAG CTC CGG GCC CGG CGC GGT CAG CGG ATC CGG CGG CCG GCG ATC
      < T   E   A   R   L   E   L   R   A   L   R   A   A   S   L   P   P   R   D

1038 CAG GTC GGT GTA CGG GGG CAC CGA GCC GCT GCC GGC GGC GGG TGC TGA GGC GTA CTG
      < L   D   T   Y   P   S   G   H   P   R   A   S   L   P   R   D

1145 CAC ACC GTC GGC CAC CTG AAC CAT CGT TAT ATT CCG GTG ACT ACC GAG CAC AGC CAC ACG CTG GCG
      > V   T   T   G   I   N   I   H   S   T   A   G   K   L   A

1235 GAC CTG GAG CGA CGG GTC GAG GCG GCG TCG GTG CGT GCC CGG TCC AAG CAG GCC AAG AAG ACG GCG CGG
      > D   L   E   R   R   V   D   E   A   V   H   A   G   S   A   R   A   R   G   K   T   A   R

1325 GAG CGG ATC GGG CTG CTC CTC GAC GAG GGG TTC GTC CAC GCC TCC CGG AAC TTC GGC CTG GAC CGC
      > E   R   I   G   L   L   L   D   E   G   F   V   H   A   R   Q   H   R   S   T   N   F   G   L   D   R

1415 ACC CGC CCG TAC CTC CTC GGC GTG ATC ACC GGC TTC GTC CTG TGC TGC CAG AGC GTC GTC TTC
      > T   R   P   Y   L   L   G   V   I   T   G   F   A   Q   D   F   T   V   F

1505 GGC GGC TCC CTC GGC GCC GAA AAG GTG ATG GAC CTG GCC TGC ATC GTC GTC GGC ATC AAC
      > G   G   S   L   G   A   E   K   I   V   K   V   M   D   L   A   M   K   I   G   C   P   V   V   G   I   N

1595 GAC GTC GGC GGC ATC TTC TTC CGC AAC GAC TTC ACC GCG CGG AGC GGC GTC
      > D   S   G   G   A   R   I   F   F   R   N   V   R   A   S   G   V

1685 ATC CCG CAG ATC TCC ATC CTG GGC GGC CCG TGC GCG GCG GTC ATG GTC GAC CAG
      > I   P   Q   I   S   I   L   M   G   P   C   A   A   V   M   V   D   Q
```

FIGURE 12A

```
1775 ACC TCG CAC ATG TTC ATC ACC GGC CCC GAC GAG GAC GTG ATC AAG ACG GTC GGT GAA CTG GGC GGT GCC CGC ACC
   >  T   S   H   M   F   I   T   G   P   D   E   D   V   I   K   T   V   G   E   L   G   G   A   R   T

1865 CAC AAC GCG CGC AGC GGC AAC GGC GAG CTG GAC GAG GAG GTG GAC GCG TAC CTC CTG TCG TAC CTG CCG
   >  H   N   A   R   S   G   N   A   E   L   D   E   E   V   D   A   Y   L   L   S   Y   L   P

1955 TCG AAC AAC TTC GAC GAG CCG CCG GTC TTC GAC GCC GAG CGG GAG CTG AGC GAC AGC CTC GTC CCG
   >  S   N   N   F   D   E   P   P   V   F   D   A   E   R   E   L   S   D   S   L   V   P

2045 GAC TCG GCG AAC GTG CAG ATG GAG TTC CTG GAG GTG CAG CCG CTG TAC GAC CAG CCG CTG TAC GCG
   >  D   S   A   N   V   Q   M   E   F   L   E   V   Q   P   L   Y   D   Q   P   L   Y   A

2135 CAG AAC GTG GTC GGT TTC CGA ATC GAG CAC CGG GTG GAG CAC CCG ATG CAC CTG ACG CTG GAC
   >  Q   N   V   V   G   F   R   I   E   H   R   V   E   H   P   M   H   L   T   L   D

2225 ATC GCG TCG ACC AAG GAG GCC GCC TGG GCG GGA CGA ATC GTC TTC GAC CTG GTG CCC GGG TTC
   >  I   A   S   T   K   E   A   A   W   A   G   R   I   V   F   D   L   V   P   G   F

2315 CTA CCC GGC ACC CGC TTC GAC GGC CAG GAG TGG GAC GGG GTG GCG TAC GAC GTG ACC CCG AAG GTC
   >  L   P   G   T   R   F   D   G   Q   E   W   D   G   V   A   Y   D   V   T   P   K   V

2405 ACC GTG ATC ACC CGC AAG ATG GGC GCG GAT CTG AAC TTC GCC GCC GTG CCG TGG CCG CGC
   >  T   V   I   T   R   K   M   G   A   D   L   N   F   A   A   V   P   W   P   R

2495 GCG CAG ATC GCG GTG ATG GGC CAG CAG GCG GCC GCG GAG GAC CCG GCC GCC GTG GCC GTG
   >  A   Q   I   A   V   M   G   Q   Q   A   A   A   E   D   P   A   A   V   A   V

2585 GCC GAG AAG ATC GCC CAG TAC GAG GAC TAC CGC GGG GTG ATC TCG AAC CAC CCG CAC CAC
   >  A   E   K   I   A   Q   Y   E   D   Y   R   G   V   I   S   N   H   P   H   H

2675 GAG ACG CGT ACC ATC GTC CGG TTG CGG GTG CTG CGC GAG ACG AAG AAC ATC CCG CTC
   >  E   T   R   T   I   V   R   L   R   V   L   R   E   T   K   N   I   P   L

2765 TAG GCGCGGTGCGGAGGGGCAGGGAGGGGCAGGGAGGGGCAGCCCCCTGTCACGCGATCCGTCACGCGATCCGGCCCCGGAGAGCCGGGGGCGGCCGGTCA GCA CGC CGG GTT
   >  •                                                                                          <  A   P   N
```

```
2878 GGC GGC GAG GCA CAT CCG CCG GGC CGT GCC GTC CTC CGC GGT GCT CTC GAG CAG TTC GCG GCC GTC GTC GAC
   <  A   A   L   C   M   R   R   A   T   R   G   E   D   S   T   E   L   L   E   R   G   D   P   G   D

2968 GCC CAA CCC GCG CTC GGG CTC ATG CGG CAG GAC GAT GAC CAG GTT GTC CTG GGT TTC CGG CAC CCC GTA GGG
   <  G   L   G   R   E   P   V   I   V   T   L   D   G   V   R   T   E   P   P   Y   G   D   V   G

3058 CTT GCC CGT CGT GGG GTC CAC CGG GGA CAT GGA CTC GCC GGC GAA GTC GAT CGT CTT CCA
   <  K   G   T   T   P   D   V   P   S   M   V   T   H   R   L   V   A   E   D   A   F   D   R   A   I   T   Q   P

3148 GGT GTG GGC CAC CGA GAT CGC CGA ACG GCC CGT GTC CAG GGG CCA GGT GCA GGT CGC GTC
   <  T   H   A   V   S   I   A   G   R   G   D   L   P   R   V   A   T   T   A   R   D

3238 CAG GTC GGC GAG GAG GTC CTG CGG GCC GGG GTC GTA GAC GAG GGG GTG CAC GTC CTT
   <  L   D   A   L   L   R   G   A   P   V   D   L   R   Y   D   Q   T   L   V   P   V   A   M   S   G   D   Q   Q

3328 CGA CGT CTC GTC CTG GGA TCG GAG CAG CAC AGA TCG AGA GTC CCC AAG CCC CAG GCC GCA CAC GTC GGC GCC
   <  S   T   D   D   L   L   T   Q   S   R   S   Y   R   S   V   P   P   G   P   E   K   G   V   A   C   S

3418 GAG CAG CAG CGG GTC CGG GTC CCC GAC GTT GCT TAC TCG CCC CTG AAG CGG GTC GGC GAC CTG CAG CAG CAG CTG
   <  L   L   P   D   V   R   V   Q   E   Q   L   G   S   D   G   L   R   V   N   S   P   V   D   A   P   D   L   L
```

FIGURE 12B

```
3508  GGC CTC CTG GCC GAT CTC GGT CCG GCC GGA CCG CTC GGT AGA CGC CTC GGT CCG GCC CCA GGA CAT CGG CGG CGC GAG GTG
      < A   E   Q   G   I   E   T   R   G   S   R   E   P   E   T   S   A   R   W   G   D   V   W   S   M   P   P   A   L   I >

3598  CCC GCC GGC CCG GCC CGC GAC GCC GCC GAA GAC CGG TAC GGC CAG CAC GGC CGC CGT ACG CCG GCT GCG
      < G   A   R   G   A   V   V   D   R   A   F   V   S   L   V   A   A   A   T   R   R   S   R >

3688  GCG GCG GCG GCG GCG GCG CGC CTC CGC GAT GTC CCG GCC GTC CAT CCG GTT CGG CGA ACG GTC AGG TCG TCA CGC
      < R   R   A   R   A   R   I   D   A   P   E   P   W   R   V   D   R   L   D   R   H   M   •   A >

3782  ATC GGC GGC CTC CTC AGA GAC GTC GAG CTC GGA GAG CGC GAG TTT CAC GGT GCC GAC CGG
      < D   A   E   E   L   D   S   V   A   L   G   A   L   R   A   K   V   T   G   V   P >

3872  GGC GGT GGC GGT CTC CTC CCG TGC CAC GGC CAC GAG CTG CGC CTC GGG CAG CCG ACG
      < A   A   T   E   R   A   V   E   A   V   P   M   G   L   L   A   E   P   L   R   R >

3962  TAG CGC CGC CAC CTC AGC GTG CGT GCT CGC CGG GAT GCT CTC CGG CGC CCG GCT ACG
      < L   A   A   V   E   L   T   A   T   S   P   A   P   V   S   E   P   A   R   L   Y   A   R   A   R   S   R >

4052  CAT GCT GCG CCA CCG GAT CGC AGC GTA CGC CTC CAC GTA CCC GCG TAC GGT CGG CCA GCG
      < M   S   R   W   R   S   V   A   I   R   S   A   V   R   L   W   G   E   P   D   Y   G   R   T   P   W   R >

4142  CTG CCA CTC GTA CGC GAA CTC GTC CGC CTG CAC GGC CAG GTT TCC GGT CAT GTA CAC GAA ACC CAG CAA TCG TTG
      < Q   W   A   R   I   Y   A   E   Q   V   A   D   Q   R   T   I   M   Y   V   F   G   L   L   R   Q >

4232  CCG GCC GCC CCG GTA GAA CTC GTC GAA CCC CTC GGC GTC CGG CAT CCGCCACCTCCCCGTGTCCAGGGGACACGCCGGGGCCCGTCGTCACGTCACGGCCGGGGGCCCCGTTGCCCGACCGG
      < R   S   G   R   Y   F   E   D   F   G   E   A   D   P   M >

4338  CCGGCTTCTTCCCTCCCCGGGGGTCTTCCCTCCCCGGGGGTCTTCCCTCCCCGGGGGTCTCCCGGGGGTCTTCCCTCCCCGGGGGTCCCGGCGCCCGTCGGGCCGGGCCTTCGG
4459  CAGCGAACAGCGACCGTCCGAGAATCGGTGTCGGCGCGGGGCCGCGGGGGCCCGGGCGGGCCGGGGCCGCGGGCCGGGGGCCGGGCCGGGCCGGGGCCGGGGGCCGGGCCGGGGCCGGGGCCGGGGCGCGGGGCCGGGGGCCGGGGGGGGCCCGGGGGCCGGGGGCCGGGGCCGGGGG

4565  GAG CAG CAG CTG CTG GCG GGC GTC GGA CTC GGA GAC GCC CAG GAA GAC CAG GAA GAC CAG GCA CTG GTG GTG TTT GTG GGC GTT CAA CCG GGC
      < L   L   L   A   G   V   A   L   G   A   D   T   L   I   P   G   A   D   T   L   I   P   G   A   L   C   V   V   L   F   V   G   V   W   F   L   P   P   P   T   L   R   R   A >

4655  GAG CTG GTC GTC GGA CTC GGA GTC CCG CAT ACG GCC GCC CGG ACG GCC GCC GAA CAG GAA
      < L   L   Q   D   A   D   S   E   P   M   R   G   R   S   R   L   R   Q   L   E   I   V   P   R   V   G   G   F   L   L   F >

4745  CCA GAC CGA GGT CCA GGC GAA CGC CGG GTA CAG CAG CCA GAC ACC GGC GGT GAT CCG GTT CCC GGC
      < W   V   S   T   W   A   F   A   A   Q   V   Q   P   P   A   Y   W   S   V   A   F   V   L   G   G   T   A   L   L   S >

4835  CAG TGC CCC GTA GAC GTT GCG GAT CAT CGC CGA CAG CAG GAT CAG CCC GGT GGG GCG GCC
      < L   A   G   Y   V   N   R   I   M   A   L   L   M   A   L   L   M   T   I   R   N   G   A >

4925  GAG CAG CCA CGC CCC GGC CAG GCG GGC GTA CCC GGC GAA CAG GGT GAG CAG CCC GGT GGG GCG GCC
      < L   L   W   A   G   A   L   G   L   T   P   A   V   Y   G   A   F   L   T   L   I   M   G   L   G   T   P   R   G >

5015  GGC CGA CAG GGT GAG CCG GTC CGA GGT GTC CGG GAG CTG CAG CTT CCG CAG GTG CAG CGC ATG ACC GCC
      < A   S   L   T   L   G   S   T   D   S   H   L   R   L   K   R   G   T   L   L   A   A   L   A   H   G   G >

5105  CTC GTG GGC GAT GGT CAC CGC GTT ACG CGC CCA GGG CAC CGC GGT GGC GTT GGC CAG GAC
      < E   H   A   I   T   V   A   N   R   A   V   R   W   P   V   R   T   A   L   V >

5195  CAG CAG CGG TGG CGG TTG CGC GGG GTC GCC GGC GAG GTC CCA GAC GCC GAT CAG CTG GAC GTC GAT CAG GCC GCA GCC TAG
      < L   L   P   P   P   D   P   P   Q   A   G   V   L   E   N   W   V   V   S   L   G   D   I   L   D   V   P   G   C   G   L >
```

FIGURE 12C

FIGURE 12D

7001 GGT CTC GGT GAG CAC CCG CAG CGC GGC CAG CGC GCG CAG CAC CCG GAA CAT GGT GTC CGC TCG GGC GTC GTA CCG CAG CGC CAA CTC CTG
     < T   E   T   L   V   R   L   A   A   L   R   F   M   T   D   A   R   D   Y   R   L   A   L   E   Q

7091 CGG GGT GCG CTC GTC CGG GAC GCC GTA GCA CCG CAT CCG GAC CCG CAG CTG GGT CGT CTC GGG GCT CGT GGC GTA CCG GGC GAA CAC CAA
     < P   T   R   E   A   D   R   Q   D   G   V   C   Y   G   A   L   R   S   A   M   G   G   F   V   L

7181 CCG CAT CAG CTC CAG GAC CTC GGC GTC GTC GCT CGT GGC GGT CTG CGC GTC CGT GGG GGC GCC GGC CTC CGT GGG CC GCTCGTCCGTGTCCGGGA
     < R   M   L   E   P   W   A   D   A   G   T   Q   C   Y   G   A   R   A   S   P   E   D   T   T   A   R   E   D   T   D   P   V

7276 CCG TCA TCG GAC CGG CGG GGC GGC CTC GGC CGG CGG CGC CGG GCG CAC GGC GCC CGT GTC GTC GAC TTC GAC CGG GTC GCC GTC GTC CAG
     < T   R   M   L   E   P   W   A   R   A   D   A   G   T   Q   C   A   R   R   A   S   P   E   D   T   T   A   R   E   D   T   D   P   V
     < M

7366 GTC CAG CTC GCC CAC CCG CAG CGC GGC GGC CTG CTG GGC CAT GAA GTC GGT GTT GGC CGT GTG GCC GGG CAC GTC CGG GAC CAG GAA GAA
     < D   L   E   G   V   P   R   V   H   A   P   L   S   P   Q   R   E   V   A   R   E   V   A   R   E   V   L   F   P

7456 GTG GCA CAG GTA GAC GTA GCA CGG GGA TCC GGT GGC GGA GAG GCG CGG GTC GCC GTC GAC GGA GTA CAC GAG GGC GCC GTA GGT GCC CTC
     < H   C   L   Y   V   D   V   A   R   G   S   A   R   G   G   E   A   S   L   P   D   R   G   V   D   L   Y   T   G   E

7546 CGG GCC GTA CGG TTC CGG CAG GTC CGG CCT CGG CGT CAG GAC GTG GAC CGC GAA CGG GAG GAG GAC ACG CTC GGT GTC GGT GTC GGA GAA
     < P   G   Y   P   E   L   L   P   P   A   E   R   V   L   T   P   A   E   R   E   D   T   D   S   F

7636 GAG GAA CAT GCC GAG CTG GGG CGC CCC CCG GCA GTT GCA CTC GTA CGC CTC CGC GCA GCG GAG GAC ACG CTC GGT GTC GGT GTC GGA GAA
     < L   F   L   L   P   V   N   P   P   A   Y   N   P   P   V   L   D   L   E   G   R   D   T   D   E

7726 CTC CCA GTT CTG GGG CTC GCC CGC CAG GTC GGC GTA GCC CCA GTC GAT ATC CAC GGC TAC GAC CCC GGC AGC GGC GTC GTC CGG GGC GCG
     < L   F   L   L   G   R   E   Q   R   S   G   R   V   D   D   A   D   I   H   W   G   Y   D   L   E   P   R

7816 CTT GGG CAC CGG GAA CCG GAA GGT TTC ACT GAA GGG CTT CGG CTG CTC GAC GTC GGA CAC CCG GGC GTG CTG CAA GGC GGC GTG
     < E   N   Q   P   R   V   P   F   T   G   F   T   Q   E   T   Q   E   P   R

7906 CAG CCG GGG CGT GGC GCT GGC CGT TTC GCC GTG GGG GCC CCG GGA CTC CGC GGT GCT CCG GTC CCA GGT   GTC   CTC   CAA   GGA   GAA
     < K   P   V   P   F   G   R   V   P   A   S   R   V   F   H   Q   V   L   Q   D   F   A   A   H

7996 GGG GTC CAT GCC GAG TTG CCA GGG TTC CAG CGC GAA CGG GAA CGC GGC CTC GCG ACC GTG GAG CGC CGC AGC AGC GAA CGT CAC GGA GAG
     < L   R   P   T   T   A   S   R   V   E   R   V   E   R   S   W   T   S   R   D   E

8086 GGA GAC CCG GAC ATG GGC CTC CTG CAG GAC CTG GCG GCT CAT CGC CAT CCG GAA TTC CGC CGG AGC CGC CTT CAC GAA CCC GTC
     < P   D   M   G   L   Q   R   A   L   E   R   D   A   P   F   A   E   L   K   V   F   G   D

8176 GTC GCA CCC GCG CTG ACC GGA CCG CTG ACC GAC GCG GCG CCT CGT CAA GAT TCG CCA GGT TGA ATG GTA GAC AAG CCG CCA GAG ACT AAC
     < S   V   F   R   E   V   Q   E   D   S   L   V   Q   A   S   M   R   A   S   M   D   R   P   P   E   G   T   N

8266 GTT TTC CTC AGC ATC GTC CGG ACC GCG AGA GCG CGG TCG CTC GCT CTC CAC CCC CCG CTC CAC CAC CCA TCA GGG TGC GGC GAT
     < N   E   A   D   D   P   G   R   S   R   R   V   G   R   E   V   R   L   W   R   S   E   G   P   A   I

8356 GCC GTC GAG CCG GGC GCG GGC CTC GAG GAA CCG CCG GTA GAC TAC CTG GTC CTG CCG GGC CGG CTG CAG CCA CGT GGG GGG GCC GAC
     < G   D   L   R   A   R   A   E   P   R   D   A   R   A   L   A   A   R   A   Q   D   L   T   R   P   G   V

8446 GAC CGT GCT CAC GGT GTA CGC CGG CCA GAC GTA GTG GCC GCC CAG CAG GGA CTC GAC CTC GAG GGC CAC CTT CGC AAA CTC GCC CAA
     < V   T   S   T   V   G   P   A   D   Y   V   V   A   H   A   L   D   P   L   S   L   G   L   E   V   A   V   K   A   L

8536 CCG GCC GGT ACG CCG GGT CGG CTG CCA CAC GTG CCG GAA GGC GTA CCG GGC GGG CGG CCG GAG GGC GTC
     < R   G   L   T   F   R   A   D   R   P   P   E   G   D
          S   P   A   Y   W   A   G   V   H   P   Q   W   H   V

FIGURE 12E

```
8626   GGC GAA CCG GTC GGA GAG CAG ACC CAT CGC CAG CGG GCT GTA GGT GAA CAG CGG CAC CAG CAC GTC CCG
        < A   F   R   D   S   L   L   G   M   A   L   P   S   Y   T   F   L   G   Y   E   A   V   D   R

8716   CTC GAT CTC GCG TTC CAG TTC CTG CAC CAC GTT CTG GGC CTC CGC GCA CAG CTG CGT CCG GGA CAG GTC GAC
        < E   I   R   E   L   L   N   Y   P   S   Q   E   A   V   P   A   G   R   S   Q   A   T   L   D   V

8806   GAT CCG CCA GCT GGG CAC CGT GTC GTA CTC GGC CAG CTG GGT CAC GTA GCG GAC CTT
        < I   R   W   S   P   V   T   G   L   E   Y   A   L   E   H   V   R   V   K

8896   GCC GCG GAC CAG GTC GAC GGA CGA CCG GAC CTC CTC AGT GTG ACG CGG GTC GAG GTC GAT GTG
        < G   S   R   V   L   D   D   L   A   S   V   T   E   E   P   R   H   L   D   I   H

8986   GTC GGT ACC CAG CCG GCG CAA CTC GCA CCG GTA CGC GGT GTC CCG TCC CGG GCC GAC CGG
        < D   T   G   L   R   R   L   S   R   E   C   K   L   A   Y   L   D   R   G   V   P

9076   ATT GAA GAT CTT GGT GGC GTC CAG CAC GCC GCC GTC CTC GAC TCC GTC GCC GCC CTG GTA GAC
        < N   F   I   K   T   A   L   L   V   D   D   R   C   S   R   G   D   Q   Y   V

9166   GTT GGC CGT GTC GAC GAG GTT GAC CTC CGC GCC GGC CTC CGG CCT GGT ACC GCC GAA GTT
        < N   A   T   D   V   L   N   V   G   A   E   V   A   I   E   E   P   G   G   F   N

9256   GAA CGC CCC CAG GGA CAC CTC TCG GTA CTG CAC CGC GTA CTC CAC GCTGCCCTCCCCCTGCGGTGGTCGCCGGCCACCC
        < F   A   G   L   S   V   K   S   V   R   L   Q   R   Y   E   V

9355   CGTCGTGCGGCCGGTGCTCCCCGAGCCCGGGAGTGGCCCGATCTCGATGGGGAGCGGGTGCTCGGCCGTTAGTACCCGCGCGGGTACTAGCAGAACTGCTAG AGC ATC CGT CGA
                                                                                                             S   I   R   R

9470   GCC GCC GGC CGG CCG AGC GGC ATG AGC CGG CGG TAC AAG TAC CGG CTG GAA CGG GGT GTG CCT GGT GTG ACG CGG GGT GTG ACC AGC GCG ATC GAG CTG
        < A   A   G   R   P   S   G   M   S   R   R   Y   K   Y   R   L   E   R   G   V   P   G   V   T   R   G   V   T   S   A   I   E   L

9560   ATC GGC GGG GAG CGG ATC AGC AGC GAC AAG TAC GTC AAC CGG CTG TGG GAA GCG CGC CAG GAG TTC TCC CGC GTG CCA CTG CAC CAC GTG GAC GAC
        < I   G   G   E   R   I   S   S   D   K   Y   V   N   R   L   W   E   A   R   Q   E   F   S   R   V   P   L   H   H   V   D   D

9650   GAC CTC ACC TCC TTC AAG TCG AGC TCC AGC GTC GAC GTG GGG GTC CGC AGC GTC TAC CTG AAG ACG CTC
        > D   L   T   S   F   K   S   S   S   S   V   D   V   G   V   R   S   V   Y   L   K   T   L

9740   ATC TTC AAC CTG GCC GAG AAC CTG GGC GAG GCC ATC CGG AAC CGG ATC GCC ATC TCC GTC
        > I   F   N   L   A   E   N   L   G   E   A   I   R   N   R   I   A   I   S   V

9830   GTC TGG GAC GGC GAC CGG ATC TGC GCG TAC GTG TAC TAT GAC TTC CTG GAG TTC CAC GTG GAC CTG GAC GGC GCG GCA
        > V   W   D   G   D   R   I   C   A   Y   V   Y   Y   D   F   L   E   F   H   V   D   L   D   G   A   D

9920   ACG GTG CTG GAG ATC GGC GCG TAC CGC TAC GCG TGT CAC AAC CAC GTC GCC TAC TTC CAC GTC GTC GAC CTG
        > T   V   L   E   I   G   A   Y   R   Y   A   C   H   N   H   D   V   A   Y   F   H   V   V   D   L

10010  CCG AAC TCC CTC GCT CTG GCC GAG GCC GTG CTC ACC GTC ACG CTG GCG GCC CAC CAC GTG GTC GGC GAG
        > P   N   S   L   A   L   A   E   A   V   L   T   V   T   L   A   R   V   H   F   H   G   V   G   E

10100  GTG GAC GGG CCG CTG AGC CCG CTG TTC GCG AGC TCG GCC GAG ATG ACG AAG AGC TGC GTG GCG GCG TAC
        > V   D   G   P   L   S   F   A   S   S   A   E   M   T   K   S   R   A   Y

10190  CTC AAC GGG TTC GTC ACC AGG CTG TAC CGC CTG TAC GTC GAC AAG AGC CTG GAC GTG GTC GAC CTG
        > L   N   G   F   V   T   R   L   Y   R   L   Y   V   D   K   S   L   D   V   V   D   L

10280  GCC GAG GTG GCC GTG GTC CGC CTG CTG TAC CAC GTC ATC CAC GAC AAC CAG CAC CGG CAG TCC
        > A   E   V   A   V   V   R   L   L   Y   H   V   I   H   D   N   Q   H   R   Q   S

10370  CGG GCG GCG TTC CTC GAC CGG AGC GTG GCG GAG AGC ATC ACG CGG TGC TGG TAC TAC TGG CAG GCG A
        > R   A   F   L   D   R   S   V   A   E   S   I   T   R   C   W   Y   Y   W   Q   A
```

FIGURE 12F

```
10460 CTC TAC CGG GCC GGC GAG GCG GCC CCG GCA CCC GGG CGG GAT TGA •
       > L   Y   R   A   G   E   A   A   P   A   P   G   R   D

10566 GGCCTGGTCGGCACCGCT GTG CTG GCC GCG CTC GCC GTC ACC GTC CGG GCC CGG GCT GCC GTG CTG CCC GCC GCG
                        > V   L   A   A   L   A   V   T   V   R   A   V   A   R   R   A   A   V   L   P   A   A

10659 CCG GGC CGC GCG TTT GAG GTG CTG GGA GCC CTG GCG GCG AAC GTC GCG GTA CGC GCG GCC GCG GTG GTC
       > P   G   R   A   F   E   V   L   G   A   L   A   A   N   V   A   V   R   A   A   V   V

10749 AAC CTC ACC CTG GAC AGT TCC GGC TGG CGG GGC GAC GAC GAC CGG TCC GCG AGC GTC ACC GAA CTC GTC GGG
       > N   L   T   L   D   S   S   G   W   R   G   D   D   D   R   S   A   S   V   T   E   L   V   G

10839 ATG CTC CGC GGG CCG GGC ACG CCC ACC CTG GTC TTC GCC GGC TCC CAG GTG GGC CGG CCC CGG ATC CCG ATC
       > M   L   R   P   G   T   P   T   L   V   F   A   G   S   Q   V   G   R   P   R   I   P   I

10929 GAC GGC ACC GAG CCG GAC CAC CCG GAT CAC CCG GCC ACC CCG TAC GAC CGG CAG CAG GCG GCC ACC GGG GCC GGC
       > D   G   T   E   P   D   H   P   A   T   P   Y   D   R   Q   Q   A   A   T   G   A   G

11019 GTC AAC GGG GTG TCG AAC GGG GTG TCC CTG CGA CTG CCC ACC GTG TTC GGC GCC CCG GTG TCC ACG ATG
       > V   N   G   V   S   N   G   V   S   L   R   L   P   T   V   F   G   A   P   V   S   T   M

11109 ATC CGC GGA GCG CTG TCC GGA GCG CAC CTG ACC ATG TGG CAC GAC GGC CGG GTG GCC GTG GCC GAC GCC GCC
       > I   R   G   A   L   S   G   A   H   L   T   M   W   H   D   G   R   V   A   V   A   D   A   A

11199 GCC TTC GTG GCG CTG GCC GCG GCC CTC GAC CAC CCG GGC GCG CTC ACC GGG GTG CTC GGT GAA CGG GAC CTG
       > A   F   V   A   L   A   A   A   L   D   H   P   G   A   L   T   G   V   L   G   E   R   D   L

11289 TTC CGC GCC ATC GCC GCC ATG GTG CTG GCC GTT GAC CGG ACC GAG CGG TCG GCC TTC GCG CCC CCG GAC GCG
       > F   R   A   I   A   A   M   V   L   A   V   D   R   T   E   R   L   A   F   A   P   P   D   A

11379 AGC GAC GTC CAC GAC GCG CTC GCC CGC CAG GCC GTC ACC GGG TGG GCG GAC CGG GTG CCG TTG CGC CTC GCG CTG GAC
       > S   D   V   H   D   A   L   A   R   Q   A   V   T   G   W   A   P   R   V   P   L   R   L   A   L   D

11469 CGC ACC GTC GAC GCG GCG TCG ATC TCC AGG CAG GTC CCG GGG CCG GAG GCC CGG ACG GCG GAT CAG GCC CGG
       > R   T   V   D   A   A   S   I   S   R   Q   V   P   G   P   E   A   P   G   A   D   Q   A   R

11553 AAG CCG GAC TCG ATC TCC AGG CAG GTC CGG TAG •
       > K   P   D   S   I   S   R   Q   V   R

11663 GTCCTCGGGGATGGGCAGGCCAGCCCGGGGTCGAGCGGCCAGTTCGTTCTCGAAGACGTACTCCTGGACAGGACGTGTCGTCGGCCGACGAAC
11784 ATGTGCGGCACCCGGACCGGCAGGTAGACCGGCCAGGTAGACCGGTAGACCGGGCAGTCCTCGTTCGAGCACCTCCGACGTCGGTGAGCACCC
11905 GGCCGTGCGGGCAGGAGACGAACTTCGCGGTGCGGGTACGGGCGGGTGAAGTGCAGCGCTTAGTGTCTCCGCGACGCGTACGCGGCCTTCGAC
12026 CCCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCGAGAGGAACACCCCCCGGTAGTCCCGGTAGCGTCAGCGGGTAGCGGCGGGGGGACACC
12147 GGCGGG
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FIGURE 12G